

10/759725

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OW protein - protein search, using sw model

Run on: December 8, 2004, 08:30:16 / Search time 187 Seconds  
(without alignments)  
15.384 Million cell updates/sec

Title: SEQ1  
Perfect score: 26  
Sequence: 1 decomp 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues  
Total number of hits satisfying chosen parameters: 47

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Uniprot 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	42.3	4	Y1M1_YEAST	P36515 saccharomyc
2	11	42.3	5	TRM3_ECOLI	P13973 escherichia
3	9	34.6	5	UC22_MAIZE	P80628 zea mays (m
4	8	30.8	5	B10A_CITR	P13071 citrobacter
5	8	30.8	5	E103_LITRU	P82099 litorea rub
6	8	30.8	5	PARP_CHICK	P83308 gallus gall
7	8	30.8	5	PRCT_PERRAM	P01131 sus scrofa
8	7	26.9	4	THYL_PIG	P19916 pseudomonas
9	7	26.9	3	DCML_PSRCH	P01858 homo sapien
10	7	26.9	4	TUPT_HUMAN	P16047 homo sapien
11	7	26.9	4	Q16047	P30425 bohrpops in
12	7	26.9	5	BEP7_BOTIN	P18644 pardachirus
13	7	26.9	5	PAP2_PARMA	P19991 acheta dome
14	7	26.9	5	SUGA_ACHDO	P24272 vibrio fisc
15	6	23.1	3	LUXE_VIRPI	P35904 achafina fu
16	6	23.1	4	ACH1_ACHFU	P58648 octopus min
17	6	23.1	4	OCPI_OCTMI	P58648 octopus min
18	6	23.1	4	OCPI_OCTMI	P58648 octopus min
19	6	23.1	5	MPA4_JUNVI	P81026 juniperus v
20	6	23.1	5	RE11_LITRU	P82072 litorea rub
21	6	23.1	5	UXA4_CHLTR	P83005 chlamydia t
22	6	23.1	5	P83073	P83073 bacillus ce
23	5	19.2	4	BOSI_HUMAN	P03721 homo sapien
24	5	19.2	4	TIME_SEPOF	P83568 sepiia offic
25	5	19.2	4	Q08433	Q08433 ratulus sp.
26	5	19.2	5	RE21_LITRU	P82071 litorea rub
27	5	19.2	5	RE31_LITRU	P82072 litorea rub
28	4	15.4	5	E104_LITRU	P82100 litorea rub
29	4	15.4	5	RE32_LITRU	P82073 litorea rub
30	4	15.4	5	TPIS_CANFA	P54714 canis famli
31	3	11.5	4	FYRI_ANTEU	P58706 anthopleura

32	3	11.5	5	1	FARP_ARTTR	P41853 artipostchi
33	3	11.5	5	1	PSK_DAUCA	P58261 daucus caro
34	3	11.5	5	1	UP01_MOUSE	P38639 mus musculu
35	2	7.7	5	2	Q99007	Q99007 hordeum vul
36	1	3.8	3	1	GRWM_HUMAN	P01157 homo sapien
37	1	3.8	4	1	DCMS_PSECH	P19948 pseudomonas
38	1	3.8	4	1	FAR3_HIRME	P42562 hirudo medi
39	1	3.8	4	1	FARA_HIRME	P42563 hirudo medi
40	1	3.8	4	1	FLRN_ANTEU	P58705 anthopleura
41	1	3.8	4	1	FLRN_ANTEU	P42561 hirudo medi
42	1	3.8	4	1	FLRN_ANTEU	P58707 anthopleura
43	1	3.8	4	1	FYRF_MACNI	P01162 macrocallis
44	1	3.8	4	2	Q96AT0	Q96AT0 homo sapien
45	1	3.8	5	1	AL14_CARMA	P81817 carcinus ma

## ALIGNMENTS

RESULT 1  
Y1M1\_YEAST STANDARD; PRT; 4 AA.  
ID Y1M1\_YEAST  
AC P36515;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Mitochondrial 60S ribosomal protein L1 (Y1M1) (Fragment).  
GN Name=Y1M1;  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91285106; PubMed=2060626;  
RA Grohmann L., Graack H.-R., Kruff V., Choi T., Goldschmidt-Reisin S.,  
RA Kitakawa M., "Extended N-terminal sequencing of proteins of the large ribosomal  
RT subunit from yeast mitochondria.",  
RL FEBS Lett. 284:51-56(1991).  
CC -!- FUNCTION: Putative component of the large subunit of mitochondrial  
CC ribosome.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
DR PIR; S17255; S17255.  
KW Direct protein sequencing; Mitochondrion; Ribosomal protein.  
FT NON TER 4  
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;  
Query Match 42.3%; Score 11; DB 1; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 VVP 5  
DB 2 VTP 4  
RESULT 2  
TRM3\_ECOLI STANDARD; PRT; 5 AA.  
ID TRM3\_ECOLI  
AC P13973;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tram protein (Fragment).  
GN Name=tram;  
OS Escherichia coli.  
OG Plasmid IncFII R100.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.

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RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshida Y., Ohtsubo E.;
RT Identification and characterization of the products from the tral and
RT tral genes of plasmid R100."
RL J. Bacteriol. 170:2749-2757(1988).
CC -1- FUNCTION: Transfer gene protein. Is involved in the conjugation
CC process of bacterial cells for the exchange of plasmid DNA.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the tral family.
CC -----
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CC -----
DR EMBL; M20941; -; NOT_ANNOTATED_CDS.
DR PIR; A32014; A32014.
KM Conjugation; DNA-binding; Plasmid.
FT NON_TER
FT SEQUENCE 5 AA; 634 MW; 6B1B1AA43500000 CRC64;
SQ

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Query Match
Best Local Similarity 42.3%; Score 11; DB 1; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DE 2
Db 3 DE 4

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RESULT 3
UC22_MAIZE STANDARD; PRT; 5 AA.
ID UC22_MAIZE
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP TISSUE=
RP TISSUE=Coleoptile;
RC TISSUE=Coleoptile;
RA Tousse P., Riccardi F., Morin C., Damerwal C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RT Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.1, its MW is: 30.4 kDa.
CC Maize-2DPAGE; P80628; COLEOPTILE.
DR Maize2DPAGE; P80628; COLEOPTILE.
DR MaizeDB; 123954; -;
KM Direct protein sequencing.
FT NON_TER
FT NON_TER
FT SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;
SQ

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Query Match
Best Local Similarity 34.6%; Score 9; DB 1; Length 5;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 EV 3
Db 4 EV 5

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RESULT 4
BIOA_CITFR STANDARD; PRT; 5 AA.
ID BIOA_CITFR
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN Name=bioA;
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8906280; PubMed=2971595;
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons."
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Biotin biosynthesis.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
CC -----
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CC -----
DR EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR PIR; 140697; 140697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; PARTIAL.
KM Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;
KM Transferase.
FT NON_TER
FT SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
SQ

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Query Match
Best Local Similarity 30.8%; Score 8; DB 1; Length 5;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DE 2
Db 4 DD 5

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RESULT 5
BIO3_LITRU STANDARD; PRT; 5 AA.
ID BIO3_LITRU
AC P82099;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 3.
OS Iltoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Iltoria.
OX NCBI_TaxID=104695;
RN [1]
RP TISSUE=
RP TISSUE=Skin secretion;

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RA Mabiniz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 630 MW; 668761P2C9A00000 CRC64;

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. NO. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVP 5
DB 2 VHP 4

RESULT 6
FARP CHICK STANDARD; PRT; 5 AA.
ID FARP CHICK
AC P83308;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE, AND SYNTHESES.
RC TISSUE=Brain;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R., Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRamide."
RL Nature 305:328-330(1983).
CC -1- FUNCTION: May function as a neurotransmitter or modulator.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO:0007218; P:neuropeptide signaling pathway; TMS.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. NO. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5
DB 1 LP 2

RESULT 7
PRCT PERAM STANDARD; PRT; 5 AA.
ID PRCT PERAM
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
OC Blattidae; Periplaneta.

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OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RN SEQUENCE.
RP SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starrett A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects."
RL Life Sci. 17:1253-1256(1975).
RN [2]
RN BIOLOGICAL SOURCE.
RP SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron."
RL Science 213:567-569(1981).
RN [3]
RN SEQUENCE.
RP SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H., III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus."
RL Peptides 11:205-211(1990).
RN [4]
RN SEQUENCE.
RP SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas."
RL Peptides 7:67-72(1986).
CC -1- FUNCTION: Stimulates cardiac output and hindgut motility,
CC modulates visceral and skeletal muscle in many arthropods.
CC -1- TISSUE SPECIFICITY: Found in the lateral white neurons and in the
CC crab pericardial organs.
DR PIR: A01644; HOROHA.
DR PIR: A60411; A60411.
KW Direct protein sequencing; Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. NO. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5
DB 3 LP 4

RESULT 8
THYL_PIG STANDARD; PRT; 3 AA.
ID THYL_PIG
AC P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protrelinin).
OS Sus scrofa (Pig).
OS Ovis aries (sheep),
OS Bombina orientalis (Oriental fire-bellied toad), and
OS Notoptalmus viridescens (Eastern newt) (Triturus viridescens).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823, 9940, 8346, 8316;
RN [1]
RN SEQUENCE.
RP SPECIES=Pig; TISSUE=Hypothalamus;
RX MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone."

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RL Biochemistry 9:1103-1106(1970).  
 RN [2]  
 RP SYNTHESES.  
 RC SPECIES=PIg;  
 RX MEDLINE=70039904; PubMed=4982117;  
 RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;  
 RT "The identity of chemical and hormonal properties of the thyrotropin  
 releasing hormone and pyroglutamyl-histidyl-proline amide.";  
 RL Biochem. Biophys. Res. Commun. 37:705-710(1969).  
 RN [3]  
 RP SPECIES=Sheep; TISSUE=Hypothalamus;  
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,  
 RT "The elucidation of the primary structure of the hypothalamic thyroid  
 stimulating hormone releasing factor of ovine origin by means of mass  
 spectrometry.";  
 RL Org. Mass Spectrom. 5:221-228(1971).  
 RN [4]  
 RP SYNTHESES.  
 RC SPECIES=Sheep;  
 RX MEDLINE=70163386; PubMed=4985794;  
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,  
 RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing  
 factor.";  
 RL Nature 226:321-325(1970).  
 RN [5]  
 RP SPECIES=Sheep;  
 RC SPECIES=B.orientalis; TISSUE=Skin;  
 RX MEDLINE=76138399; PubMed=815011;  
 RA Yasuhara T., Nakajima T.;  
 RT "Occurrence of pyr-his-pro-nh2 in the frog skin.";  
 RL Chem. Pharm. Bull. 23:3301-3303(1975).  
 RN [6]  
 RP SPECIES=N.viridescens;  
 RX MEDLINE=75035605; PubMed=4214528;  
 RA Grimm-Joergensen Y., McKelvy J.F.;  
 RT "Biosynthesis of thyrotropin releasing factor by new (Triturus  
 viridescens) brain in vitro. Isolation and characterization of  
 thyrotropin releasing factor.";  
 RL J. Neurochem. 23:471-478(1974).  
 CC -1- FUNCTION. TSH functions as a regulator of the biosynthesis of TSH  
 in the anterior pituitary gland and as a neurotransmitter/  
 neuromodulator in the central and peripheral nervous systems.  
 CC PIR; A90919; RHTDIO.  
 DR PIR; A92971; A92971.  
 DR PIR; A93750; RHSH.  
 KM Annotation: Direct protein sequencing; Pyrolytic carboxylic acid.  
 FT MOD\_RRS 1 1 Pyrolytic carboxylic acid.  
 FT MOD\_RRS 3 3 Proline amide.  
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;  
 Query Match 26.9%; Score 7; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 P 5  
 DB 3 P 3  
 RESULT 9  
 DCM1\_PSECH STANDARD; PRT; 4 AA.  
 AC P19916;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
 dehydrogenase subunit L) (CO-DH L) (Fragment).  
 GN Name=culL;

OS Pseudomonas carboxydohydrogena.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae.  
 OX NCBI\_TaxID=290;  
 RN [1]  
 RP SPECIES=Sheep;  
 RX MEDLINE=90055678; PubMed=2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
 RT "Homology and distribution of CO dehydrogenase structural genes in  
 RT carboxydohydrogena.";  
 RL Arch. Microbiol. 152:335-341(1989).  
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
 dioxide.  
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
 CC -1- COPACOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1  
 CC molybdopterin cytosine dinucleotide (MCD) per subunit.  
 CC -1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
 CC subunit.  
 DR PIR; PL0140; PL0140.  
 KM Direct protein sequencing; Molybdenum; Oxidoreductase.  
 FT NON TER 4  
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F000000000 CRC64;  
 Query Match 26.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 P 5  
 DB 4 P 4  
 RESULT 10  
 TUFT\_HUMAN STANDARD; PRT; 4 AA.  
 AC P01858;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Phagocytosis-stimulating peptide (tuftsin).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SPECIES=Sheep;  
 RX MEDLINE=72187087; PubMed=4112769;  
 RA Nishio K., Constantopoulos A., Satoh P.S., Najjar V.A.;  
 RT "The characteristics, isolation and synthesis of the phagocytosis  
 stimulating peptide tuftsin.";  
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).  
 RN [2]  
 RP IMMUNOGLOBULIN CLAS.  
 RX MEDLINE=68091045; PubMed=4169272;  
 RA Fidalgo B.V., Najjar V.A.;  
 RT "The physiological role of the lymphoid system. VI. The stimulatory  
 RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic  
 RT activity of human polymorphonuclear leucocyte.";  
 RL Biochemistry 6:3386-3392(1967).  
 CC -1- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the  
 CC cell membrane of neutrophils in the blood. Leucokininase on the  
 CC membrane releases the active peptide tuftsin from the gamma chain.  
 CC Tuftsin is essential for maximum stimulation of the phagocytic  
 CC activity of neutrophils.  
 DR PIR; A02147; A02147.  
 DR MIM; 191150; -.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006909; P:phagocytosis; NAS.  
 KM Direct protein sequencing.  
 SQ SEQUENCE 4 AA; 501 MW; 74176321C000000000 CRC64;  
 Query Match 26.9%; Score 7; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 P 5  
 1  
 Db 3 P 3

## RESULT 11

Q16047 PRELIMINARY; PRT; 4 AA.  
 ID 016047  
 AC 016047;  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)  
 DE Interleukin 2 receptor alpha-subunit (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxId=9606;  
 RX MEDLINE=92062171; PubMed=1840490;  
 RP SEQUENCE FROM N.A.  
 RA Dautry-Varot A., Colline M., Mayaux J.F.;  
 RT "An exon 5-deleted mRNA encodes a functional interleukin 2 receptor  
 alpha-subunit.";  
 RT Biochem. Biophys. Res. Commun. 180:1390-1395(1991).  
 DR EMBL; S64248; AAB20279.1;  
 DR GO; GO:0005525; F:GTP binding; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0007264; F:small GTPase mediated signal transduction; IEA.  
 DR InterPro; IPR001806; Ras\_trnsmfmg.  
 DR Pfam; PF00071; Ras; 1.  
 DR PRINTS; PRO0449; RASTRNSFRMG.  
 DR GTP-binding; Receptor.  
 KW NON\_TER 4  
 FT SEQUENCE 4 AA; 525 MW; 69CAB769A0000000 CRC64;  
 SQ

Query Match 26.9%; Score 7; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5  
 1  
 Db 2 P 2

RESULT 12  
 BPP7\_BOTIN STANDARD; PRT; 5 AA.  
 ID BPP7\_BOTIN  
 AC P30425;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting  
 enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 OC Viperidae; Crotalinae; Bothrops.  
 NCBI\_TaxId=8723;  
 RX MEDLINE=90351557; PubMed=238615;  
 RC TISSUE=Venom;  
 RA Cintrá A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 angiotensin-converting enzyme and enhances the action of  
 bradykinin by inhibiting the kinases that inactivate it. It acts  
 as an indirect hypotensive agent.

DR PIR; G37196; G37196.  
 KW Direct protein sequencing; Hypotensive agent;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1  
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5  
 1  
 Db 5 P 5

## RESULT 13

PAR2\_PARMA STANDARD; PRT; 5 AA.  
 ID PAR2\_PARMA  
 AC P81864;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pardaxin II (PXII) (Fragment).  
 OS Pardaxin marmoratus (Red sea moses sole).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;  
 OC Soleiidae; Soleidae; Pardaxinus.  
 NCBI\_TaxId=31087;  
 RX MEDLINE=87057369; PubMed=3782138;  
 RP TISSUE=Skin secretion;  
 RA Lazarovici P., Primor N., Loew L.M.;  
 RT "Purification and pore-forming activity of two hydrophobic  
 polypeptides from the secretion of the Red sea moses sole (Pardaxinus  
 marmoratus).";  
 RT J. Biol. Chem. 261:16704-16713(1986).  
 CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant  
 properties. Forms voltage-dependent, ion-permeable channels in  
 membranes. At high concentration causes cell membrane lysis.  
 CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
 CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
 CC -1- SIMILARITY: Belongs to the pardaxin family.  
 KW Direct protein sequencing; Toxin.  
 FT NON\_TER 5  
 SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5  
 1  
 Db 5 P 5

## RESULT 14

SUGA\_ACHDO STANDARD; PRT; 5 AA.  
 ID SUGA\_ACHDO  
 AC P1991;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Suboesophageal ganglion pentapeptide.  
 OS Acheta domestica (House cricket).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
 OC Acheta.  
 NCBI\_TaxId=6997;  
 RX MEDLINE=6997;  
 RP SEQUENCE.  
 RA Wicker C., Wicker C.;

RT "Isolation and structure of a peptide isolated from the subesophageal  
 RT ganglion of Acheata domestica (Orthoptera)."  
 RL Comp Biochem Physiol. 88C:185-187(1987).  
 CC -1- SUBCELLULAR LOCATION: Main peptide from the subesophageal  
 CC ganglia.  
 DR PIR: J50319; J50319.  
 DR Direct protein sequencing.  
 SQ SEQUENCE 5 AA; 476 MW; 69D76DDDD80000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 P 5  
 DB 4 P 4

RESULT 15  
 LUXE\_VIBF1  
 ID LUXE\_VIBF1 STANDARD; PRT; 3 AA.  
 AC P24272;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl)-  
 DE protein synthetase) (Fragment).  
 GN Name=luxe;  
 OS Vibrio fischeri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91072226; PubMed=2254256;  
 RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;  
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination  
 RT site for the lux operon."  
 RL J. Bacteriol. 172:6797-6802(1990).  
 CC -1- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It  
 CC is a component of the fatty acid reductase complex responsible for  
 CC converting tetradecanoic acid to the aldehyde which serves as  
 CC substrate in the luciferase-catalyzed reaction.  
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +  
 CC an acyl-protein thioester.  
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.  
 CC -1- SIMILARITY: Belongs to the luxe family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M62812; -; NOT\_ANNOTATED\_CDS.  
 DR Ligase; Luminescence.  
 KM NON\_TER 1  
 FT 1  
 SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D 1  
 DB 3 D 3

Search completed: December 8, 2004, 08:51:54  
 Job time : 190 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 8, 2004, 08:31:09 ; Search time 159 Seconds  
(without alignments)  
11.281 Million cell updates/sec

Title: SEQ1  
Perfect score: 26  
Sequence: 1 devvp 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	5	4	AAB66374
2	26	100.0	5	5	ABG31916
3	26	100.0	5	7	ABU61522
4	26	100.0	5	7	ABU61519
5	26	100.0	6	4	AAM52534
6	26	100.0	6	4	AAB67389
7	26	100.0	6	4	AAB66359
8	26	100.0	6	4	AAB66377
9	26	100.0	6	4	AAB66384
10	26	100.0	6	4	AAG64159
11	26	100.0	6	5	ABG31912
12	26	100.0	6	5	ABG31915
13	26	100.0	6	5	ABR05374
14	26	100.0	6	5	ABG32506
15	26	100.0	6	5	ABG32506
16	26	100.0	9	6	ABG74004
17	26	100.0	9	6	ABG74003
18	26	100.0	58	1	AAP81263
19	26	100.0	72	1	AAP50049
20	26	100.0	74	1	AAP50047
21	26	100.0	74	1	AAP82689
22	26	100.0	75	1	AAP71201
23	26	100.0	78	4	AAE09778
24	26	100.0	96	4	AAU45914
25	26	100.0	96	6	ABM42433

26	26	100.0	98	8	ADP99245	Adp99245
27	26	100.0	100	6	ABM71931	Abm71931
28	26	100.0	108	4	AAU42592	Aau42592
29	26	100.0	108	6	ABM39111	Abm39111
30	26	100.0	108	6	ABM65718	Abm65718
31	26	100.0	120	4	AAE02771	Aae02771
32	26	100.0	120	4	AAU57682	Aau57682
33	26	100.0	120	6	ABM54201	Abm54201
34	26	100.0	120	8	ADQ30924	Adq30924
35	26	100.0	125	8	AAE82656	Aae82656
36	26	100.0	125	8	ADJ71222	Adj71222
37	26	100.0	126	1	AAE50037	Aae50037
38	26	100.0	126	1	AAE51240	Aae51240
39	26	100.0	126	2	AAE00582	Aae00582
40	26	100.0	126	2	AAW34533	Aaw34533
41	26	100.0	128	8	ADP99246	Adp99246
42	26	100.0	130	7	ADD71229	Add71229
43	26	100.0	130	7	ADD71230	Add71230
44	26	100.0	130	7	ADD71231	Add71231
45	26	100.0	130	8	ADJ71224	Adj71224

## ALIGNMENTS

RESULT 1	
ABM66374	standard; peptide; 5 AA.
ID	ABM66374:
AC	09-APR-2001 (first entry)
DT	Hepatitis C virus protease inhibitor boronic acid peptide #20.
XX	Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
DE	liver cancer; NS3; antiviral agent.
KW	Synthetic.
XX	
OS	
XX	
FM	Key
FT	Modified-site
FT	1 /label= OTHER
FT	/note= "optionally Boc-Asp(OtBu) or Ac-Asp(OtBu)"
FT	Modified-site
FT	2 /label= OTHER
FT	/note= "Glu(OtBu)"
XX	
FM	WO200102424-A2.
XX	11-JAN-2001.
PD	
XX	07-JUL-2000; 2000WC-US018655.
PF	
XX	07-JUL-1999; 99US-0142561P.
PR	
XX	(DUPO ) DU PONT PHARM CO.
PA	
XX	Ketner CA, Jagannathan S, Forsyth TP;
PI	WPI, 2001-103001/11.
XX	
DR	New boronic acid derivatives, optionally containing peptides, used to
XX	treat hepatitis C infections, are hepatitis C viral protease inhibitors.
PT	
PT	Example 9; Page 127; 258pp; English.
XX	
PS	The present invention provides a number of boronic acid derivatives which
CC	act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
CC	be used to treat infection by the virus, which can cause liver cirrhosis
CC	and liver cancer
XX	
XX	Sequence 5 AA;
SQ	

Query Match 100.0%; Score 26; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 |||||  
 1 DEVVP 5

RESULT 2  
 ABG31916

ID ABG31916 standard; peptide; 5 AA.

XX AC ABG31916;

XX DT 05-NOV-2002 (first entry)

XX DE HCV serine protease imidazolidinone inhibitor #2.

XX KW HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;  
 XX KW hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;  
 XX KW viral infection; blood plasma processing.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT Misc-difference 2 /note= "OTHER= Boc-Asp (OCBu) "

FT Modified-site 5 /note= "Glu(OCBu) "

FT /label= OTHER

FT /note= "OTHER= Hydroxyl group"

XX PN W0200248157-A2.

XX PD 20-JUN-2002.

XX PF 12-DEC-2001; 2001WO-US047916.

XX PR 13-DEC-2000; 2000US-0255168P.

XX PA (BRIM ) BRISTOL MYERS SQUIBB PHARMA CO.

XX PI Han Q;

XX DR WPI; 2002-559498/64.

XX PT New imidazolidinones useful as serine protease inhibitors in the  
 XX treatment of e.g. viral infection.

XX PS Example 20; Page 115; 173pp; English.

XX CC This invention relates to novel imidazolidinones or their stereoisomers,  
 CC salts or prodrugs which are useful as serine protease inhibitors. The  
 CC imidazolidinones of the invention may have virucide, hepatotropic, or  
 CC antiinflammatory activities and may be used as a serine protease  
 CC inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or  
 CC a HCV growth inhibitor. Compounds of the invention are useful for  
 CC treating viral infection e.g. hepatitis C virus (HCV) infection and as a  
 CC reagent used as inhibitors of HCV protease in the processing of blood  
 CC plasma for diagnostic and other commercial purposes. The imidazolidinones  
 CC of the invention inhibit HCV NS3 protease and/or HCV growth and thus can  
 CC be used in the blood plasma assay. The present sequence represents a  
 CC imazolidinone protease inhibitor shown in the examples of the  
 CC specification

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 |||||  
 1 DEVVP 5

RESULT 3  
 ABU61522

ID ABU61522 standard; peptide; 5 AA.

XX AC ABU61522;

XX DT 08-AUG-2003 (first entry)

XX DE Hepatitis C virus NS3 protease inhibitor peptide.

XX KW Hepatitis C virus; NS3 protease; hepatotropic; virucide;  
 XX KW antiinflammatory; serine protease inhibitor; hepatitis C virus;  
 XX KW NS3 Protease inhibitor; viral infection; elastase; chymotrypsin.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /label= O-CBu (not defined)

FT Modified-site 1 /note= "Boc (not defined) "

FT Modified-site 2 /note= "O-CBu (not defined) "

FT Modified-site 5 /note= "C-terminal hydroxyl"

XX PN US2002177725-A1.

XX PD 28-NOV-2002.

XX PF 28-OCT-2001; 2001US-00039317.

XX PR 23-OCT-2000; 2000US-0242557P.

XX PA (PRIE/) PRIESTLEY E S.

XX PI Priestley ES;

XX DR WPI; 2003-465950/44.

XX PT New class of peptides are inhibitors of hepatitis C virus NS3 protein,  
 XX useful for treating e.g. hepatitis.

XX PS Example 1; Page 27; 54pp; English.

XX CC The invention describes novel peptide useful for treating viral  
 CC infections e.g. Hepatitis C virus (HCV) infections. The compounds have  
 CC HCV NS3 protease inhibitory selectivity over inhibition of elastase and  
 CC chymotrypsin. This is the amino acid sequence of a modified peptide  
 CC associated with an assay of NS3 protease activity

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 7; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 |||||  
 1 DEVVP 5

RESULT 4

ABU61519

ID ABU61519 standard; peptide; 5 AA.

XX





Best local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
Db 1 DEVVP 5

## RESULT 6

AAB67389 ID AAB67389 standard; peptide; 6 AA.

AC AAB67389;

DT 26-APR-2001 (first entry)

DE Protease inhibitor.

KW Lactam; hepatitis C virus; HCV; NS3 protease.

OS Synthetic.

PN WO200107407-A1.

PD 01-FEB-2001.

PF 26-JUL-2000; 2000WO-US020189.

PR 26-JUL-1999; 99US-0145631P.

PA (DUPO ) DU PONT PHARM CO.

PI Priestley ES, Decicco CP;

DR WPI; 2001-159696/16.

PT New lactam derivatives are hepatitis C virus NS3 protease inhibitors  
PT useful for treating HCV infections.

PS Example 26; Page 100; 130pp; English.

CC The present invention relates to lactam derivatives. These derivatives  
CC may be used for treating hepatitis C virus (HCV) infection. They can also  
CC be used for inhibiting HCV in a body fluid sample and as a standard or  
CC reagent in a test or assay for determining the ability of a potential  
CC pharmaceutical to inhibit HCV NS3 protease and/or HCV growth

XX Sequence 6 AA;

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
Db 1 DEVVP 5

## RESULT 7

AAB66359 ID AAB66359 standard; peptide; 6 AA.

AC AAB66359;

DT 09-APR-2001 (first entry)

DE Hepatitis C virus protease inhibitor boronic acid peptide #9.

KW Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;

KW liver cancer; NS3; antiviral agent.

OS Synthetic.

XX

FH Key Location/Qualifiers  
FT Modified-site 1

FT /label= OTHER

FT /note= "optionally Boc-Asp (OtBu), Ac-Asp (OtBu) or Ac-Asp"

FT Modified-site 2

FT /label= OTHER

FT /note= "optionally Glu (OtBu), optionally D-form residue"

FT Modified-site 6

FT /label= OTHER

FT /note= "optionally boro-L-2-amino-3-cyclopropylpropionic

FT (borocpa) acid pinanediol ester. borocpa pinanediol,

FT boroCpa pinanediol ester.Hcl, boro-L-2-amino-4-pentenoic

FT acid (borocalg) pinanediol, boroAlg pinanediol

FT ester.trifluoroacetate, boroAlg-ClOH16, boroAlg, boroApe-

FT pinanediol, boroApe-pinanediol.Hcl, boro-L-4,4'-difluoro-

FT 1-amino-butyric acid (borodfb) pinanediol or borodfb

FT pinanediol ester.hydrochloride"

FT WO200102424-A2.

PN 11-JAN-2001.

PD 07-JUL-2000; 2000WO-US018655.

PF 07-JUL-1999; 99US-0142561P.

PR (DUPO ) DU PONT PHARM CO.

PA Kettner CA, Jagannathan S, Forsyth TP;

PI WPI; 2001-103001/11.

DR New boronic acid derivatives, optionally containing peptides, used to

XX treat hepatitis C infections, are hepatitis C viral protease inhibitors.

PT Example 7; Page 255; 258pp; English.

PS The present invention provides a number of boronic acid derivatives which

CC act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can

CC be used to treat infection by the virus, which can cause liver cirrhosis

CC and liver cancer

XX Sequence 6 AA;

XX Query Match 100.0%; Score 26; DB 4; Length 6;

XX Best local Similarity 100.0%; Pred. No. 1.7e+06;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 DEVVP 5

Db 1 DEVVP 5

XX RESULT 8

AAB6377 ID AAB6377 standard; peptide; 6 AA.

AC AAB6377;

DT 09-APR-2001 (first entry)

DE Hepatitis C virus protease inhibitor boronic acid peptide #23.

XX Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;

XX liver cancer; NS3; antiviral agent.

XX Synthetic.

OS Key Location/Qualifiers

XX Modified-site 1 /label= OTHER

XX Modified-site 2 /note= "optionally Boc-Asp (OtBu)"

FT

FT	/label= OTHER
FT	/note= "optionally Glu(OtBu) "
FT	Modified-site
FT	6
FT	/label= OTHER
FT	/note= "optionally borovinylgly pinanediol ester,
FT	borocyclopropylglycine pinanediol ester or
FT	borocyclopropylglycine pinanediol ester Hcl"
XX	
PN	WO200102424-A2.
XX	
PD	11-JAN-2001.
XX	
PF	07-JUN-2000; 2000WO-US018655.
XX	
PR	07-JUL-1999; 99US-0142561P.
XX	
PA	(DUPO ) DU PONT PHARM CO.
XX	
PI	Kettner CA, Jagannathan S, Forsyth TP;
XX	
DR	WPI; 2001-103001/11.
XX	
PT	New boronic acid derivatives, optionally containing peptides, used to
PT	treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX	
PS	Example 15; Page 132; 256pp; English.
XX	
CC	The present invention provides a number of boronic acid derivatives which
CC	act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
CC	be used to treat infection by the virus, which can cause liver cirrhosis
CC	and liver cancer
XX	
SQ	Sequence 6 AA;
	Query Match 100.0%; Score 26; DB 4; Length 6;
	Best Local Similarity 100.0%; Pred. 1.7e+06;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 DEVVP 5
Dd	1 DEVVP 5
RESULT 9	
AAB66384	
ID AAB66384 standard; peptide; 6 AA.	
XX	
AC AAB66384;	
XX	
DT 09-APR-2001 (first entry)	
XX	
DE Hepatitis C virus protease inhibitor boronic acid peptide #30.	
XX	
KM Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;	
KW liver cancer; NS3; antiviral agent.	
XX	
OS Synthetic.	
XX	
FH Key Location/Qualifiers	
FT Modified-site 1	
FT	/label= OTHER
FT	/note= "optionally Boc-Asp(OtBu) "
FT	2
FT Modified-site	
FT	/label= OTHER
FT	/note= "optionally Glu(OtBu) "
FT	6
FT	/label= OTHER
FT	/note= "optionally boroser(Obz1) pinanediol,
FT	boroser(Obz1)-ClOH16, boroser pinanediol, boroser(Obz1)
FT	pinanediol Hcl or boroser pinanediol Hcl"
XX	
PN WO200102424-A2.	
XX	

PD	11-JAN-2001.
XX	
PF	07-JUL-2000; 2000MO-US018655.
PR	07-JUL-1999; 99US-0142561P.
XX	
PA	(DUPO ) DU PONT PHARM CO.
XX	
PI	Kettner CA, Jagannathan S, Forsyth TP;
DR	WPI; 2001-103001/11.
XX	
PT	New boronic acid derivatives, optionally containing peptides, used to treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX	
PS	Example 46; Page 154; 258pp; English.
CC	The present invention provides a number of boronic acid derivatives which act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can be used to treat infection by the virus, which can cause liver cirrhosis and liver cancer
XX	
SQ	Sequence 6 AA:
Query Match	100.0%; Score 26; DB 4; Length 6;
Best Local Similarity	100.0%; Pred. No. 1.7e+06;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 DEVP 5       1 DEVP 5
Db	

RESULT 10
AAG64159
ID AAG64159 standard; peptide; 6 AA.
XX
AC AAG64159;
XX
DT 19-OCT-2001 (first entry)
XX
DE HCV NS3 protease inhibitor.
XX
KW Hepatitis C virus; HCV; NS3 protease; alpha-ketoamide inhibitor;
KM virinidic; hepatotropic; antiinflammatory; viral infection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6
PT /note= "boroAlg"
XX
PN WO200140262-A1.
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000MO-US032677.
XX
PR 03-DEC-1999; 99US-016898P.
XX
PA (DUPO ) DU PONT PHARM CO.
XX
PI Han W;
XX
DR WP1; 2001-464936/50.
XX
PT New ketoamide derivatives useful for treating infections e.g. hepatitis C
PT virus.
XX
PS Disclosure; Page 195; 282pp; English.
XX
CC The invention relates to novel ketoamide and ketoester derivatives for
CC use as inhibitors of hepatitis C virus (HCV) NS3 protease inhibitors. The

CC compounds are useful for treating viral infections e.g. hepatitis C  
CC virus. The present sequence was used to inhibit hydrolysis of an ester  
CC substrate by HCV NS3 protease  
XX  
80 Sequence 6 AA;

QY	1 DEVVP 5
Db	1 DEVVP 5
RESULT 11	
ABG31912	
ABG31912 standard; peptide; 6 AA.	
ABG31912,	
05-NOV-2002 (first entry)	
HCV NS4a serine protease inhibitor peptide.	
HCV, hepatitis C; imidazolidinone; serine protease inhibitor; virucide; hepatotropic; antiinflammatory; NS3 protease; growth inhibitor; viral infection; blood plasma processing.	
Synthetic.	
Key	Location/Qualifiers
Modified-site	1
	/label= OTHER
	/note= "OTHER= Hydrogenated"
Modified-site	6
	/label= OTHER
	/note= "OTHER= Hydroxyl group"
Misc-difference	6
	/label= OTHER
	/note= "OTHER= boro-Alg, L-2-amino-4-pentenoic acid - boronic acid"
WO200248157-A2.	
20-JUN-2002.	
12-DEC-2001; 2001WO-US047916.	
13-DEC-2000; 2000US-0255168P.	
(BRIM ) BRISTOL MYERS SQUIBB PHARMA CO.	
Han Q;	
WPI; 2002-599498/64.	
New imidazolidinones useful as serine protease inhibitors in the treatment of e.g. viral infection.	
Example 20; Page 112; 173pp; English.	
This invention relates to novel imidazolidinones or their stereoisomers, salts or prodrugs which are useful as serine protease inhibitors. The imidazolidinones of the invention may have virucide, hepatotropic, or antiinflammatory activities and may be used as a serine protease inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or a HCV growth inhibitor. Compounds of the invention are useful for treating viral infection e.g. hepatitis C virus (HCV) infection and as a plasma for diagnostic and other commercial purposes. The imidazolidinones of the invention inhibit HCV NS3 protease and/or HCV growth and thus can be used in the blood plasma assay. The present sequence represents an HCV	

CC NS4a serine protease inhibitor shown in the examples of the specification  
XX  
SQ Sequence 6 AA;

```

RESULT 12
ABG31919
ID ABG31919 standard; peptide; 6 AA.
XX
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE HCV serine protease imidazolidinone inhibitor #5.
XX
KW HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;
XX hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;
XX viral infection; blood plasma processing.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Boc-Asp(OtBu)"
FT Misc-difference 2 /label= Glu(OtBu)
FT Misc-difference 6 /note= "L-2-amino-4-pentenoic acid-boronic acid"
FT Modified-site 6 /label= OTHER
FT /note= "OTHER= pinane diol labelled"
XX
PN WO200248157-A2.
XX
PD 20-JUN-2002.
XX
PF 12-DEC-2001; 2001WO-US047916.
XX
PR 13-DEC-2000; 2000US-0255168P.
XX
PA (BRIM ) BRISTOL MYERS SQUIBB PHARMA CO.
XX
PI Han Q;
XX
DR WPI; 2002-599498/64.
XX
XX New imidazolidinones useful as serine protease inhibitors in the
PT treatment of e.g. viral infection.
PT
XX
XX Example 20; Page 118; 173pp; English.
XX
XX This invention relates to novel imidazolidinones or their stereoisomers,
CC salts or prodrgs which are useful as serine protease inhibitors. The
CC antiinflammatory activities and may be used as a serine protease
CC inhibitor (preferably hepatitis C virus (HCV) NS3 protease inhibitor) or
CC a HCV growth inhibitor. Compounds of the invention are useful for
CC treating viral infection e.g. hepatitis C virus (HCV) infection and as a
CC reagent used as inhibitors of HCV protease in the processing of blood
CC plasma for diagnostic and other commercial purposes. The imidazolidinones
CC be used in the blood plasma assay. The present sequence represents a
CC imazolidinone protease inhibitor shown in the examples of the
CC specification
XX

```

PT New indazoleidionones useful as serine protease inhibitors in the  
 PT treatment of e.g. viral infection.  
 XX  
 XX  
 PS Example 20; Page 118; 173pp; English.  
 XX  
 CC This invention relates to novel indazoleidionones or their stereoisomers,  
 CC salts or prodrugs which are useful as serine protease inhibitors. The  
 CC indazoleidionones of the invention may have a virucide, hepatotropic, or  
 CC antiinflammatory activities and may be used as a serine protease  
 CC inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or  
 CC a HCV growth inhibitor. Compounds of the invention are useful for  
 CC treating viral infections e.g. hepatitis C virus (HCV) infection and as a  
 CC reagent used as inhibitors of HCV protease in the processing of blood  
 CC plasma for diagnostic and other commercial purposes. The indazoleidionones  
 CC of the invention inhibit HCV NS3 protease and/or HCV growth and thus can  
 CC be used in the blood plasma assay. The present sequence represents a  
 CC indazoleidionone protease inhibitor shown in the examples of the  
 CC specification  
 XX

PT New indazoleidionones useful as serine protease inhibitors in the  
PT treatment of e.g. viral infection.  
XX  
XX  
PS Example 20; Page 118; 173pp; English.  
XX  
XX This invention relates to novel indazoleidionones or their stereoisomers,  
CC salts or prodrugs which are useful as serine protease inhibitors. The  
CC indazoleidionones of the invention may be used as a serine protease  
CC antiinflammatory activities and may be used as a serine protease  
CC inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or  
CC a HCV growth inhibitor. Compounds of the invention are useful for  
CC treating viral infection e.g. hepatitis C virus (HCV) infection and as a  
CC reagent used as inhibitors of HCV protease in the processing of blood  
CC plasma for diagnostic and other commercial purposes. The indazoleidionones  
CC of the invention inhibit HCV NS3 protease and/or HCV growth and thus can  
CC be used in the blood plasma assay. The present sequence represents a  
CC indazoleidionone protease inhibitor shown in the examples of the  
XX specification

SQ Sequence 6 AA:

Query Match 100.0%; Score 26; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 |||||  
 DB 1 DEVVP 5

RESULT 13

ABG31915

ID ABG31915 standard; peptide; 6 AA.

AC ABG31915;

XX 05-NOV-2002 (first entry)

DE HCV serine protease imidazolidinone inhibitor #1.

XX HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;

KM hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;

XX viral infection; blood plasma processing.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT /note= "OTHER=Hydrogenated"

FT Misc-difference 10 /label= OTHER

FT /note= "OTHER= L-2-amino-4-pentonic acid- boronic acid-  
 pinane diol ester-trifluoroacetate"

XX MO200248157-A2.

XX 20-JUN-2002.

XX 12-DEC-2001; 2001WO-US047916.

XX 13-DEC-2000; 2000US-0255168P.

XX (BRIM ) BRISTOL MYERS SQUIBB PHARMA CO.

XX Han Q;

XX WPI; 2002-599498/64.

XX New imidazolidinones useful as serine protease inhibitors in the  
 treatment of e.g. viral infection.

XX Example 20; Page 115; 173pp; English.

XX This invention relates to novel imidazolidinones or their stereoisomers,  
 CC salts or prodrugs which are useful as serine protease inhibitors. The  
 CC imidazolidinones of the invention may have virucide, hepatotropic, or  
 CC antiinflammatory activities and may be used as a serine protease  
 CC inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or  
 CC a HCV growth inhibitor. Compounds of the invention are useful for  
 CC treating viral infection e.g. hepatitis C virus (HCV) infection and as a  
 CC reagent used as inhibitors of HCV protease in the processing of blood  
 CC plasma for diagnostic and other commercial purposes. The imidazolidinones  
 CC of the invention inhibit HCV NS3 protease and/or HCV growth and thus can  
 CC be used in the blood plasma assay. The present sequence represents a  
 CC imazolidinone protease inhibitor shown in the examples of the  
 CC specification

SQ Sequence 6 AA:

Query Match 100.0%; Score 26; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 |||||  
 DB 1 DEVVP 5

RESULT 14

ABB05374

ID ABB05374 standard; peptide; 6 AA.

AC ABB05374;

XX 08-APR-2002 (first entry)

DE Peptide Q9714.

XX Hepatitis C virus; HCV; hepatitis C protease NS3; inhibitor; nocotropic;

KM neuroprotective; tranquilliser; anticonvulsant; virucide; hepatotropic;

XX antiinflammatory; hepatitis C infection; neurological disorder; epilepsy;

KM anxiety; insomnia; Alzheimer's disease.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 6 /note= "A1GCF2CF3"

XX MO200196540-A2.

XX 20-DEC-2001.

XX 08-JUN-2001; 2001WO-US018751.

XX 11-JUN-2000; 2000US-0210900P.

XX (DUPO ) DUPONT PHARM CO.

XX Kettner CA, Hixon MS;

XX WPI; 2002-154599/20.

XX Novel binding site of NS3:NS4A complex characterized by binding of a  
 specific sequence, useful for the discovery of inhibitors of hepatitis C  
 protease and the treatment of hepatitis C disease.

XX Disclosure; Page 17; 46pp; English.  
 CC The present invention describes a binding site (I) of hepatitis C  
 CC protease (NS3):NS4A complex characterized by binding of a sequence (S),  
 CC where binding is inhibitory when measured by enzymatic hydrolysis of a  
 CC peptide substrate encompassing P6-P7' binding sites, and non-inhibitory  
 CC when measured by enzymatic hydrolysis of a peptide substrate encompassing  
 CC P6-P2' binding sites but does not extend into P4'-P7' binding sites  
 CC region. (I) has nocotropic, neuroprotective, tranquilliser, virucide,  
 CC anticonvulsant, hepatotropic and antiinflammatory activities. (I) is  
 CC useful for the discovery of inhibitors of hepatitis C protease and the  
 CC treatment of hepatitis C disease. Inhibitors of hepatitis C can also be  
 CC used for treating neurological disorders related to modulation of a  
 CC potassium channel, more specifically the M-current, formed by expression  
 CC of KCNQ2 and KCNQ3 genes, such as epilepsy, anxiety, insomnia or  
 CC Alzheimer's disease. The present sequence represents a peptide which is  
 CC used in the exemplification of the present invention

SQ Sequence 6 AA:

Query Match 100.0%; Score 26; DB 5; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 |||||  
 DB 1 DEVVP 5

```

RESULT 15
ABG32506
ID ABG32506 standard; peptide; 6 AA.
XX
XX ABG32506;
AC
XX
XX 15-NOV-2002 (first entry)
DT
XX
XX Peptide inhibitor for HCV NS3 protease.
DE
XX
XX NS3; HCV; protease; HCV infection; hepatitis; cirrhosis; liver cancer;
KM pyrimidinone; serine protease inhibitor; virucide; hepatotropic;
XX antiinflammatory; blood plasma processing.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "Asp is hydrogenated"
FT
FT Modified-site 6 /note= "BoroAlg residue"
FT
XX
XX WO200248116-A2.
XX
XX 20-JUN-2002.
XX
XX 12-DEC-2001; 2001WO-US047911.
XX
XX 13-DEC-2000; 2000US-0255290P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB PHARMA CO.
XX
XX Glunz FW, Doucy BD, Han W;
XX
XX WPI; 2002-627251/67.
XX
XX New pyrimidinones useful as serine protease inhibitors in the treatment
XX of e.g. viral infection.
XX
XX Example 140; Page 191; 270pp; English.
XX
XX The invention relates to pyrimidinones of a formula given in the claims
XX of the specification, their stereoisomers, salts and prodrugs. In assays,
XX the pyrimidinone compounds inhibited Hepatitis C virus (HCV) NS3 protease
XX with IC50 values of less than 100 micro M. The compounds are useful for
XX treating viral infection e.g. HCV infection (the causative agent of acute
XX hepatitis and associated with cirrhosis and liver cancer) and as a
XX reagent used as inhibitors of HCV protease in the processing of blood
XX plasma for diagnostic and other commercial purposes. The present sequence
XX is a peptide inhibitor used to determine NS3 concentration in assays
XX described in the specification
XX
XX Sequence 6 AA;
SQ

```

```

Query Match 100.0%; Score 26; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DEVVP 5
   |||||
Db 1 DEVVP 5

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Search completed: December 8, 2004, 08:54:39  
 Job time : 162 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - protein search, using SW model

Run on: December 8, 2004, 08:30:16 : Search time 149 Seconds  
(without alignments)  
12.038 Million cell updates/sec

Title: SEQ1  
Perfect score: 26  
Sequence: 1 deerp 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 43520

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	26	100.0	5 4 AAB66374	Aab66374 Hepatitis
2	26	100.0	5 5 ABG31916	ABg31916 HCV serin
3	26	100.0	5 7 ABU61522	ABu61522 Hepatitis
4	26	100.0	5 7 ABU61519	ABu61519 Hepatitis
5	21	80.8	5 4 AAB66355	Aab66355 Hepatitis
6	20	76.9	4 4 AAM52537	Aam52537 NS3 prote
7	20	76.9	4 4 AAB66375	Aab66375 Hepatitis
8	20	76.9	4 4 ABG31917	ABg31917 HCV serin
9	20	76.9	4 5 ABG31918	ABg31918 HCV serin
10	20	76.9	5 4 AAB66364	Aab66364 Hepatitis
11	20	76.9	5 7 ABU61524	ABu61524 Hepatitis
12	19	73.1	4 2 AAR44221	Aar44221 Tyrosinas
13	19	73.1	4 2 AAR58582	Aar58582 N termina
14	19	73.1	4 4 AAB66373	Aab66373 Hepatitis
15	18	69.2	4 2 AAM73297	Aam73297 HL60 cell
16	18	69.2	5 8 AD070448	Ado70448 Trp-contra
17	17	65.4	4 2 AAR44222	Aar44222 Tyrosinas
18	17	65.4	4 2 AAR58583	Aar58583 N termina
19	17	65.4	5 3 AAR33073	Aar33073 Protein t
20	17	65.4	5 8 AD070480	Ado70480 Trp-contra
21	17	65.4	5 8 AD070446	Ado70446 Trp-contra
22	17	65.4	5 8 AAR65523	Aar65523 Endothei
23	16	61.5	5 2 AAY15685	Aay15685 Peptide u
24	16	61.5	5 3 AAY80839	Aay80839 Fluoropho
25	16	61.5	5 3 AAY80839	Aay80839 Fluoropho

26	16	61.5	5 4 AAG66393	Aag66393 Azapeptid
27	16	61.5	5 8 AD070478	Ado70478 Trp-contra
28	15	57.7	4 2 AAR48289	Aar48289 ACE inhib
29	15	57.7	4 2 AAR88260	Aar88260 Intermedi
30	15	57.7	4 2 AAR88264	Aar88264 Intermedi
31	15	57.7	4 2 AAR88263	Aar88263 Intermedi
32	15	57.7	4 2 AAR88262	Aar88262 Intermedi
33	15	57.7	4 2 AAR88261	Aar88261 Intermedi
34	15	57.7	4 2 AAR88266	Aar88266 Intermedi
35	15	57.7	4 2 AAM93984	Aam93984 Antineopl
36	15	57.7	4 2 AAM93985	Aam93985 Antineopl
37	15	57.7	4 2 AAM66250	Aam66250 ICE pepti
38	15	57.7	4 2 AAM76200	Aam76200 Mouse cas
39	15	57.7	4 2 AAM52756	Aam52756 Aminometh
40	15	57.7	4 2 AAM48940	Aam48940 Apopain (
41	15	57.7	4 2 AAM66735	Aam66735 Dolastaci
42	15	57.7	4 2 AAM56305	Aam56305 Peptide c
43	15	57.7	4 2 AAM48948	Aam48948 Apopain (
44	15	57.7	4 2 AAM66566	Aam66566 Peptide u
45	15	57.7	4 2 AAM66566	Aam66566 Peptide u

## ALIGNMENTS

RESULT 1	
AAB66374	AAB66374 standard; peptide; 5 AA.
XX	XX
AC	AAB66374;
XX	XX
DT	09-APR-2001 (first entry)
DE	Hepatitis C virus protease inhibitor boronic acid peptide #20.
XX	Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
XX	KW liver cancer; NS3; antiviral agent.
XX	XX
OS	Synthetic.
XX	XX
PH	Key
FT	Modified-site 1 Location/Qualifiers
FT	/label= OTHER
FT	/note= "optionally Boc-Asp(OtBu) or Ac-Asp(OtBu) "
FT	Modified-site 2 /label= OTHER
FT	/note= "Glu(OtBu) "
XX	XX
PN	W0200102424-A2.
XX	XX
PD	11-JAN-2001.
XX	XX
PP	07-JUL-2000; 2000WO-US018655.
XX	XX
PR	07-JUL-1999; 99US-0142561P.
XX	XX
PA	(DUPO ) DU POINT PHARM CO.
XX	XX
PI	Kettner CA, Jagannathan S, Forsyth TP;
XX	XX
DR	WPI; 2001-103001/11.
XX	XX
PT	New boronic acid derivatives, optionally containing peptides, used to
XX	XX
PS	treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX	XX
XX	Example 9: Page 127; 258pp; English.
XX	XX
CC	The present invention provides a number of boronic acid derivatives which
CC	be used as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
CC	be used to treat infection by the virus, which can cause liver cirrhosis
CC	and liver cancer
XX	XX
SQ	Sequence 5 AA;

Query Match	100.0%	Score 26	DB 4	Length 5
Best Local Similarity	100.0%	Pred. NO. 1.7e+06		
Matches	5	Conservative 0	Mismatches 0	Indels 0
Qy	1	DEVP 5		
Db	1	DEVP 5		

RESULT 2	ABG31916
ID	ABG31916 standard; peptide; 5 AA.
XX	
AC	ABG31916;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	HCV serine protease imidazolinone inhibitor #2.
XX	
KW	HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide
KW	hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;
KW	viral infection; blood plasma processing.
XX	
OS	Synthetic.
XX	

Key	Location/Qualifiers
Modified-site	1
	/label= OTHER
Misc-difference	/note= "OTHER= Boc-Asp(OtBu) "
	2
Modified-site	/note= "Glu(OtBu) "
	5
	/label= OTHER
	/note= "OTHER= Hydroxy] group"

PN WO200248157-A2

PD 20-JUN-2002

PF 12-DEC-2001; 2001WO-US047916.  
XX

13-DEC-2000; 2000US-0255168P.

PA (BRIM ) BRISTOL MYERS SQUIBB PHARMA CO.  
XX

Han Q;

WPI; 2002-599498/64.

PT New imidazolidinones useful as serine protease inhibitors in the treatment of e.g. viral infection.

Example 20; Page 115; 173pp; English.

This invention relates to novel imidazolidinones or their stereoisomers, salts or prodrugs which are useful as serine protease inhibitors. The imidazolidinones of the invention may have virucide, hepatotropic, or antiinflammatory activities and may be used as a serine protease inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or a HCV growth inhibitor. Compounds of the invention are useful for treating viral infection e.g. hepatitis C virus (HCV) infection and as a reagent used as inhibitors of HCV protease in the processing of blood plasma for diagnostic and other commercial purposes. The imidazolidinones of the invention inhibit HCV NS3 protease and/or HCV growth and thus can be used in the blood plasma assay. The present sequence represents a imazolidinone protease inhibitor shown in the examples of the specification.

Sequence 5 AA;

Query Match	100.0%;	Score 26;	DB 5;	Length 5;
Best Local Similarity	100.0%;	Pred. No. 1.7e+06;		

	Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	DEVVP	5							
Db	1	DEVVP	5							

RESULT 3	
ABU61522	
ID	ABU61522 standard; peptide; 5 AA.
XX	
AC	ABU61522;
XX	
DT	08-AUG-2003 (first entry)
XX	

Hepatitis C virus NS3 protease inhibitor peptide  
XX

KW antinflammatory: serine protease inhibitor; hepatitis C virus; NS3 protease; hepatotropic; virucide;

XX  
NM  
NS3  
XX

protease inhibitor; viral infection; elastase; chymotrypsin

synthetic.

FT	Modified-site	Location/Qualifiers
in	key	

Modified-site	1	/label= O-tBu (not defined)
FT		

FT	Modified-site	/note= "Boc (not defined)"
2	2	

FT	Modified-site	5	/note= "O-CBU (not defined)
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/ note= "C-terminal hydroxyl"

XX 00200211123-AL

**X**

XX  
2004-0003551/

XX 2000, 200005-024255/F

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[illegible]

new class of peptides are inhibitors of hepatitis C virus NS3 protein, useful for treating e.g. hepatitis.

Example 1; Page 27; 54pp; English.

The invention describes novel peptide useful for treating viral infections e.g. Hepatitis C virus (HCV) infections. The compounds have HCV NS3 protease inhibitory selectivity over inhibition of elastase and chymotrypsin. This is the amino acid sequence of a modified peptide associated with an assay of NS3 protease activity

Sequence 5 AA;

Query Match	100.0%;	Score 26;	DB 7;	Length 5;
Best Local Similarity	100.0%;	Pred. No. 1.7e+06;		
Matches	5;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

2y	1	DEVP	5
2b	1	DEVP	5

## RESULT 4

ABU61519 standard; peptide; 5 AA



AC	ABU61519;	
XX		
DT	08-AUG-2003	(first entry)
XX		
DE	Hepatitis C virus NS3 protease inhibitor.	
XX		
KW	Hepatitis C virus; NS3 protease; hepatotropic; virucide; antiinflammatory; serine protease inhibitor; hepatitis C virus; NS3 Protease Inhibitor; viral infection; elastase; chymotrypsin.	
XX		
OS	Synthetic.	
XX		
Key	Location/Qualifiers	
Modified-site	5	
FT	/note= "(1R)-1-amino-3-phenylpropylboronic acid (+)-	
FT	pinaneediol ester, or (1R)-1-amino-4-phenylbutylboronic	
FT	acid (+)-pinaneediol ester, (1R)-amino-5-	
FT	phenylbutylboronic acid (+)- pinaneediol ester, or (1R)-1-	
FT	amino-3-(2- naphthyl)propylboronic acid (+)-pinaneediol	
FT	ester, or (1R)-1-amino-3-(2-methyl) phenylpropylboronic	
FT	acid (+)-pinaneediol ester, or (1R)-1-amino-3-(3-	
FT	methyl)phenylpropylboronic acid (+)-pinaneediol ester, or	
FT	(1R)-1-amino-3-(4-methyl)phenylpropylboronic acid (+)-	
FT	pinaneediol ester, or (1R)-1-amino-3-(1,1'- biphényl)-4-	
FT	propylboronic acid (+)- pinaneediol ester, or (1R)-1-	
FT	amino-3-(2,5-dimethyl) phenylpropylboronic acid (+)-	
FT	pinaneediol ester, or (1R)-1-amino-3-(2,4-	
FT	dimethyl)phenylpropylboronic acid (+)-pinaneediol ester, or	
FT	(1R)-1-amino-3-(4- trifluoromethyl)phenylpropylboronic	
FT	acid (+) pinaneediol ester, or (1R)-1-amino-3-(3-	
FT	trifluoromethyl)phenylpropylboronic acid (+)- pinaneediol	
FT	ester, or (1R)-1-amino-3-(4-fluoro) phenylpropylboronic	
FT	acid (+) pinaneediol ester, or (1R)-1-amino-3-	
FT	(4phenoxy)phenylpropylboronic acid (+)-pinaneediol ester,	
FT	or (1R)-1-amino-3-(4- isopropyl)phenylpropylboronic acid	
FT	(+)-pinaneediol ester, or (1R)-1-amino-3-(4-cyclohexyl)	
FT	phenylpropylboronic acid (+)- pinaneediol ester, or (1R)-1-	
FT	amino-3-(4-tert-butyl) phenylpropylboronic acid (+)-	
FT	pinaneediol ester, or (1R)-1-amino-3-(4-	
FT	methoxy)phenylpropylboronic acid (+)-pinaneediol ester, or	
FT	(1R)-1-amino-3-(4- chloro)phenylpropylboronic acid (+)-	
FT	pinaneediol ester, or (1R)-1-amino-3-(4-bromo)	
FT	phenylpropylboronic acid (+)-pinaneediol ester, or (1R)-1-	
FT	amino-3-(2-fluoro)phenylpropylboronic acid (+)-pinaneediol	
FT	ester, or (1R)-1-amino-3-(3-fluoro)phenylpropylboronic	
FT	acid (+)-pinaneediol ester, or (1R)-1-amino-3-(2,6-	
FT	difluoro) phenylpropylboronic acid (+)- pinaneediol ester,	
FT	or (1R)-1-amino-3-(4-hydroxy)phenylpropylboronic acid (+)-	
FT	pinaneediol ester, or (1R)-1- aminohexylboronic acid (+)-	
FT	pinaneediol ester, or (1R)-1-amino-5-methylhexylboronic	
FT	acid (+)- pinaneediol ester, or (1R)-1-aminohexylboronic	
FT	acid (+)- pinaneediol ester, or (1R)-1-amino-4-	
FT	cyclobutylbutylboronic acid (+)- pinaneediol ester, or (1R)-	
FT	-1-amino-5-ethylheptylboronic acid (+)- pinaneediol ester	
FT	1R is not defined."	
XX		
PN	US2002177725-A1.	
XX		
PD	28-NOV-2002.	
XX		
PF	28-OCT-2001; 2001US-00039317.	
XX		
PR	23-OCT-2000; 2000US-0242557P.	
XX		
PA	(PRIE/) PRIESTLEY E S.	
XX		
PI	Priestley ES;	
XX		
DR	WPI: 2003-465950/44.	
XX		
PT	New class of peptides are inhibitors of hepatitis C virus NS3 protein,	
XX	useful for treating e.g. hepatitis.	

```

PS      Example; Page 14-15; 54pp; English.
XX
XX      The invention describes novel peptide useful for treating viral
CC      infections e.g. Hepatitis C virus (HCV) infections. The compounds have
CC      HCV NS3 protease inhibitory selectivity over inhibition of elastase and
CC      chymotrypsin. This is the amino acid sequence of a modified peptide that
CC      functions as an NS3 inhibitor
XX
XX      Sequence 5 AA;
SQ
      Query Match          100.0%;      Score 26;  DB 7;  Length 5;
      Best Local Similarity 100.0%;      Pred. No. 1.7e+06;
      Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
QY      1 DEVVP 5
      |||||
      1 DEVVP 5
DB
      RESULT 5
      AAB6355
      ID AAB66355 standard; peptide; 5 AA.
      XX
      AC AAB66355;
      XX
      XX 09-APR-2001 (first entry)
      DT
      DE Hepatitis C virus protease inhibitor boronic acid peptide #5.
      XX
      KM Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
      KW liver cancer; NS3; antiviral agent.
      OS Synthetic.
      XX
      XX Key Location/Qualifiers
      FH Modified-site 3 /label= OTHER
      FT /note= "2-methyl-phenylalanine"
      FT Modified-site 4 /label= OTHER
      FT /note= "3-methyl-valine"
      FT
      XX MO200102424-A2.
      XX
      XX 11-JAN-2001.
      PD
      XX 07-JUL-2000; 2000WO-US018655.
      PF
      XX 07-JUL-1999; 99US-0142561P.
      PR
      XX (DUPO ) DU PONT PHARM CO.
      PA
      XX Ketner CA, Jagannathan S, Forsyth TP;
      PI WPI, 2001-103001/11.
      DR
      XX New boronic acid derivatives, optionally containing peptides, used to
      PT treat hepatitis C infections, are hepatitis C viral protease inhibitors.
      PR
      XX Claim 8; Page 11; 258pp; English.
      PS
      XX The present invention provides a number of boronic acid derivatives which
      CC act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
      CC be used to treat infection by the virus, which can cause liver cirrhosis
      CC and liver cancer
      XX
      XX Sequence 5 AA;
SQ
      Query Match          80.8%;      Score 21;  DB 4;  Length 5;
      Best Local Similarity 80.0%;      Pred. No. 1.7e+06;
      Matches 4;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
QY      1 DEVVP 5

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Db          1 DEFPV 5
RESULT 6
AAMS2537
ID AAMS2537 standard; peptide; 4 AA.
XX
AC AAMS2537;
XX
DT 31-JAN-2002 (first entry)
XX
DE NS3 protease peptide inhibitor #2.
XX
KM Virucide; pyrrolopyrazinone derivative; Hepatitis C virus inhibitor;
XX nonstructural 3 protease; NS3 protease; viral infection.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="Optionally Z-Glu(OtBu) or H-Glu(OtBu)"
FT Modified-site 4 /note="Optionally Pro-OBzl or Pro-OH"
XX
PN WO200164678-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006269.
XX
PR 29-FEB-2000; 2000US-0185618P.
XX
PA (DUPO ) DUPONT PHARM CO.
XX
PI Zhang X, Han W;
XX
DR WPI; 2001-656752/75.
XX
FT New pyrrolopyrazinone derivatives useful for treating Hepatitis C virus
PT infection are NS3 protease inhibitors.
XX
PS Disclosure; Page 134; 191pp; English.
XX
CC The present invention relates to a novel pyrrolopyrazinone derivative,
CC its stereoisomer or salt. It was found that the derivative is a Hepatitis
CC C virus (HCV) nonstructural (NS) 3 protease inhibitor. The derivative is
CC useful for the manufacture of a medicament for the treatment of HCV and
CC in therapy for treating HCV infection. The present peptide is a peptide
CC inhibitor for HCV NS3 protease, which was used to illustrate the present
CC invention
XX
SQ Sequence 4 AA;
Query Match 76.9%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EVVP 5
Db 1 EVVP 4
RESULT 7
AAB6375
ID AAB6375 standard; peptide; 4 AA.
XX
AC AAB6375;
XX
DT 09-APR-2001 (first entry)
XX
DE Hepatitis C virus protease inhibitor boronic acid peptide #21.
XX

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KM Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
KM liver cancer; NS3; antiviral agent.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT Modified-site 1 /note="Optionally Glu(OtBu) or Ac-Glu(OtBu)"
XX
PN WO200102424-A2.
XX
PD 11-JAN-2001.
XX
PF 07-JUL-2000; 2000WO-US018655.
XX
PR 07-JUL-1999; 99US-0142561P.
XX
PA (DUPO ) DU PONT PHARM CO.
XX
PI Kettner CA, Jagannathan S, Forsyth TP;
XX
DR WPI; 2001-103001/11.
XX
PT New boronic acid derivatives, optionally containing peptides, used to
PT treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX
PS Example 9; Page 128; 258pp; English.
XX
CC The present invention provides a number of boronic acid derivatives which
CC act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
CC be used to treat infection by the virus, which can cause liver cirrhosis
CC and liver cancer
XX
SQ Sequence 4 AA;
Query Match 76.9%; Score 20; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EVVP 5
Db 1 EVVP 4
RESULT 8
ABG31917
ID ABG31917 standard; peptide; 4 AA.
XX
AC ABG31917;
XX
DT 05-NOV-2002 (first entry)
XX
DE HCV serine protease imidazolinone inhibitor #3.
XX
KM HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;
KM hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;
KM viral infection; blood plasma processing.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Glu(OtBu)"
FT Modified-site 1 /label= OTHER
FT Modified-site 4 /note= "OTHER= Hydrogenated"
FT Modified-site 4 /label= OTHER
FT /note= "OTHER= Hydroxy" group"
XX
PN WO200248157-A2.
XX

```

PD 20-JUN-2002.  
 XX 12-DEC-2001; 2001WO-US047916.  
 PF 13-DEC-2000; 2000US-0255168P.  
 XX  
 XX (BRIM ) BRISTOL MYERS SQUIBB PHARMA CO.  
 PA  
 XX Han Q;  
 PI  
 PS WPI; 2002-599498/64.  
 DR  
 XX New imidazolidinones useful as serine protease inhibitors in the  
 XX treatment of e.g. viral infection.  
 PT  
 PS Example 20; Page 117; 173pp; English.  
 XX  
 XX This invention relates to novel imidazolidinones or their stereoisomers,  
 XX salts or prodrugs which are useful as serine protease inhibitors. The  
 XX imidazolidinones of the invention may have virucide, hepatotropic, or  
 XX antiinflammatory activities and may be used as a serine protease  
 XX inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or  
 XX a HCV growth inhibitor. Compounds of the invention are useful for  
 XX treating viral infection e.g. hepatitis C virus (HCV) infection and as a  
 XX reagent used as inhibitors of HCV protease in the processing of blood  
 XX plasma for diagnostic and other commercial purposes. The imidazolidinones  
 XX of the invention inhibit HCV NS3 protease and/or HCV growth and thus can  
 XX be used in the blood plasma assay. The present sequence represents a  
 XX imazolidinone protease inhibitor shown in the examples of the  
 XX specification  
 SQ  
 XX Sequence 4 AA;  
 QY  
 Query Match 76.9%; Score 20; DB 5; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 2 EVVP 5  
 1 EVVP 4  
 Db  
 RESULT 9  
 ABG31918  
 ID ABG31918 standard; peptide; 4 AA.  
 AC  
 XX ABG31918;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE HCV serine protease imidazolinone inhibitor #4.  
 XX  
 XX HCV; hepatitis C; imidazolidinone; serine protease inhibitor; virucide;  
 KM hepatotropic; antiinflammatory; NS3 protease; growth inhibitor;  
 KM viral infection; blood plasma processing.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /label= Z  
 FT /note= "Z-Glu(OtBu)"  
 FT Modified-site 4 /note= "Pro-Obz1"  
 FT  
 XX  
 XX W0200248157-A2.  
 EN  
 XX 20-JUN-2002.  
 PD  
 XX 12-DEC-2001; 2001WO-US047916.  
 PF  
 XX 13-DEC-2000; 2000US-0255168P.  
 PR  
 XX

PA (BRIM ) BRISTOL MYERS SQUIBB PHARMA CO.  
 XX  
 XX Han Q;  
 PI  
 PS WPI; 2002-599498/64.  
 DR  
 XX New imidazolidinones useful as serine protease inhibitors in the  
 XX treatment of e.g. viral infection.  
 PT  
 PS Example 20; Page 117; 173pp; English.  
 XX  
 XX This invention relates to novel imidazolidinones or their stereoisomers,  
 XX salts or prodrugs which are useful as serine protease inhibitors. The  
 XX imidazolidinones of the invention may have virucide, hepatotropic, or  
 XX antiinflammatory activities and may be used as a serine protease  
 XX inhibitor (preferably Hepatitis C virus (HCV) NS3 protease inhibitor) or  
 XX a HCV growth inhibitor. Compounds of the invention are useful for  
 XX treating viral infection e.g. hepatitis C virus (HCV) infection and as a  
 XX reagent used as inhibitors of HCV protease in the processing of blood  
 XX plasma for diagnostic and other commercial purposes. The imidazolidinones  
 XX of the invention inhibit HCV NS3 protease and/or HCV growth and thus can  
 XX be used in the blood plasma assay. The present sequence represents a  
 XX imazolidinone protease inhibitor shown in the examples of the  
 XX specification  
 SQ  
 XX Sequence 4 AA;  
 QY  
 Query Match 76.9%; Score 20; DB 5; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 2 EVVP 5  
 1 EVVP 4  
 Db  
 RESULT 10  
 AAB66364  
 ID AAB66364 standard; peptide; 5 AA.  
 AC  
 XX AAB66364;  
 XX  
 DT 09-APR-2001 (first entry)  
 XX  
 DE Hepatitis C virus protease inhibitor boronic acid peptide #14.  
 XX  
 XX Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;  
 KM liver cancer; NS3; antiviral agent.  
 KM  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /label= OTHER  
 FT /note= "C-terminal acetyl, optionally Glu(OtBu)"  
 FT Modified-site 5 /label= OTHER  
 FT /note= "optionally boro-L-2-amino-4-pentenoic acid  
 FT (boroxalg) pinanediol or boroxalg-cl0H16"  
 FT  
 XX  
 XX W0200102424-A2.  
 EN  
 XX 11-JAN-2001.  
 PD  
 XX 07-JUL-2000; 2000WO-US018655.  
 PF  
 XX 07-JUL-1999; 99US-0142561P.  
 PR  
 XX (DUPO ) DU PONT PHARM CO.  
 PA  
 XX Kettner CA, Jagannathan S, Forsyth TP;  
 PI  
 XX WPI; 2001-103001/11.  
 DR

XX New boronic acid derivatives, optionally containing peptides, used to  
 PT treat hepatitis C infections, are hepatitis C viral protease inhibitors.  
 XX  
 XX Example 33; Page 256; 2588p; English.  
 XX  
 CC The present invention provides a number of boronic acid derivatives which  
 CC act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can  
 CC be used to treat infection by the virus, which can cause liver cirrhosis  
 CC and liver cancer  
 XX  
 SQ Sequence 5 AA;

Query Match 76.9%; Score 20; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
 ||||  
 DB 1 EIVP 4

RESULT 11  
 AB061524  
 ID AB061524 standard; peptide; 5 AA.  
 AC AB061524;  
 DT 08-AUG-2003 (first entry)

DE Hepatitis C virus NS3 protease enzyme assay associated peptide #4.  
 KW Hepatitis C virus; NS3 protease; hepatotropic; virucide;  
 KW antiinflammatory; serine protease inhibitor; hepatitis C virus;  
 KW NS3 Protease Inhibitor; viral infection; elastase; chymotrypsin.  
 XX Synthetic.

OS  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 5  
 FT /note= "borolag (not defined)-C-terminal hydroxy"]"

PN US2002177725-A1.  
 XX  
 PD 28-NOV-2002.  
 XX  
 PF 28-OCT-2001; 2001US-00039317.  
 XX  
 PR 23-OCT-2000; 2000US-0242557P.  
 XX

PA (PRIE/) PRIESTLEY E S.  
 XX  
 PT Priestley ES;  
 XX  
 DR WPI; 2003-465950/44.  
 XX

PT New class of peptides are inhibitors of hepatitis C virus NS3 protein,  
 PT useful for treating e.g. hepatitis.  
 XX  
 PS Example 39; Page 39; 54p; English.  
 XX

CC The invention describes novel peptide useful for treating viral  
 CC infections e.g. Hepatitis C virus (HCV) infections. The compounds have  
 CC HCV NS3 protease inhibitory selectivity over inhibition of elastase and  
 CC chymotrypsin. This is the amino acid sequence of a modified peptide  
 CC associated with an assay of NS3 protease activity  
 XX

SQ Sequence 5 AA;

Query Match 76.9%; Score 20; DB 7; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
 ||||  
 DB 2 EIVP 5

RESULT 12  
 AAR44221  
 ID AAR44221 standard; peptide; 4 AA.  
 AC AAR44221;  
 XX

DT 03-JUN-1994 (first entry)

DE Tyrosinase (N-terminus).

KW Tyrosine; inhibic; tyrosinase; drugs; cosmetics; foods; pesticide;  
 KW vermin.

OS Musca domestica.  
 XX

PN JP05287000-A.  
 XX

PD 02-NOV-1993.  
 XX

PF 09-APR-1992; 92JP-00089148.  
 XX

PR 09-APR-1992; 92JP-00089148.  
 XX

PA (SAMP) SANSHO PHARM CO LTD.  
 XX

DR WPI; 1993-383080/48.  
 XX

PT New peptide having high tyrosinase inhibiting activity - useful for  
 PT drugs, cosmetics, foods and pesticidal agents.  
 XX

PS Claim 1; Page 2; 9p; Japanese.  
 XX

CC The sequences (AAR44221-22) show the possible N-terminus of a novel  
 CC tyrosinase. The peptide is useful in the production of drugs, cosmetics,  
 CC foods and pesticidal agents  
 XX

SQ Sequence 4 AA;

Query Match 73.1%; Score 19; DB 2; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
 ||||  
 DB 1 EIVP 4

RESULT 13

ID AAR58582 standard; peptide; 4 AA.  
 XX

AC AAR58582;  
 XX

DT 25-APR-1995 (first entry)

DE N terminal fragment of peptide inhibitor of tyrosinase activity.  
 XX

KW tyrosinase inhibitory peptide; medicine; cosmetics; agrochemicals;  
 KW N terminal fragment; insecticides; extraction from living body.  
 XX

OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "H-Glu"

PN JP06220085-A.  
 XX

```

PD 09-AUG-1994.
XX
XX 09-APR-1992; 92JP-00089147.
XX
XX 09-APR-1992; 92JP-00089147.
XX
XX (SIYA ) SANSEI SEIYAKU KK.
XX
XX WPI; 1994-290910/36.
XX
XX New tyrosinase inhibitory peptide - for use in medicine, cosmetics and
XX agrochemicals.
XX
XX Claim 1; Page 2; 9pp; Japanese.
XX
XX AAR58582 is an N-terminal fragment of a tyrosinase inhibitory peptide.
XX
XX The inhibitory peptide is useful in medicines, cosmetics, extraction from
XX agrochemicals, etc. It is prepared from known methods, eg. extraction from
XX a living body, synthetic methods, genetic recombination, etc. (see also
XX AAR58583)
XX
XX Sequence 4 AA:
SQ
Query Match 73.1%; Score 19; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 EVVP 5
   |||
   1 EIVP 4
Db
RESULT 14
AAB6373
ID AAB6373 standard; peptide; 4 AA.
XX
XX AAB6373;
XX
XX 09-APR-2001 (first entry)
XX
XX Hepatitis C virus protease inhibitor boronic acid peptide #19.
XX
XX Hepatitis C virus; protease; boronic acid; inhibitor; liver cirrhosis;
XX liver cancer; NS3; antiviral agent.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /label= OTHER
XX Modified-site 2 /note= "Boc-Asp(OtBu)"
XX Modified-site 2 /label= OTHER
XX Modified-site 2 /note= "Glu(OtBu)"
XX
XX WO200102424-A2.
XX
XX 11-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US018655.
XX
XX 07-JUL-1999; 99US-0142561P.
XX
XX (DUPO ) DU PONT PHARM CO.
XX
XX Kettner CA, Jagannathan S, Forsyth TP;
XX
XX WPI; 2001-103001/11.
XX
XX New boronic acid derivatives, optionally containing peptides, used to
XX treat hepatitis C infections, are hepatitis C viral protease inhibitors.
XX
XX Example 7; Page 123; 258pp; English.

```

```

XX
XX The present invention provides a number of boronic acid derivatives which
XX act as inhibitors of the hepatitis C virus NS3 protease enzyme. They can
XX be used to treat infection by the virus, which can cause liver cirrhosis
XX and liver cancer
XX
XX Sequence 4 AA:
SQ
Query Match 73.1%; Score 19; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVV 4
   |||
   1 DEVV 4
Db
RESULT 15
AAW73297
ID AAW73297 standard; peptide; 4 AA.
XX
XX AAW73297;
XX
XX 08-FEB-1999 (first entry)
XX
XX HL60 cell line protein fragment.
XX
XX HL60; human; staurosporine; neurodegenerative disease; neuropathy;
XX immunodeficiency; geriatric disease; transplant rejection; therapy;
XX hyperproliferative disease; autoimmune disease; dermatological disease.
XX
XX Homo sapiens.
XX
XX WO9845429-A2.
XX
XX 15-OCT-1998.
XX
XX 14-APR-1998; 98WO-EP002157.
XX
XX 10-APR-1997; 97GB-00007307.
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERM GES MBH.
XX
XX Imfeld D, Fuerst P, Schindler P, Maerki W;
XX
XX WPI; 1998-568349/48.
XX
XX Polypeptides from the HL60 cell line - used to treat neurodegenerative
XX diseases e.g. neuropathies, immunodeficiencies, geriatric disease.
XX
XX Example 7; Page 30; 50pp; English.
XX
XX This sequence represents a fragment of a polypeptide of the invention.
XX The polypeptides were isolated from the HL60 cell line. The polypeptide
XX can be used as a drug, or as a marker or surrogate marker for monitoring
XX a cellular condition or disease achievable by application of
XX staurosporine. They can also be used for identification of a drug for
XX treatment of a disease selected from disease responsive to induction of a
XX cellular condition achievable by application of staurosporine, and
XX diseases responsive to inhibition of a cellular condition achievable by
XX application of staurosporine. The diseases include neurodegenerative
XX diseases, neuropathies, immunodeficiencies, geriatric disease, transplant
XX rejection diseases, hyperproliferative diseases, autoimmune diseases and
XX dermatological diseases
XX
XX Sequence 4 AA:
SQ
Query Match 69.2%; Score 18; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 EVVP 5

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Wed Dec 8 10:04:34 2004

seq1.closed.rag

Page 8

DB 1 RIP 4

Search completed: December 8, 2004, 08:33:38  
Job time : 152 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 8, 2004, 08:30:16 / Search time 37 Seconds  
(without alignments)  
8.962 Million cell updates/sec

Title: SEQ1  
Perfect score: 26  
Sequence: 1 decomp 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 26504

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_6/prodata/1/aa/5A.COMB.pep.\*  
2: /cgn2\_6/prodata/1/aa/5B.COMB.pep.\*  
3: /cgn2\_6/prodata/1/aa/6A.COMB.pep.\*  
4: /cgn2\_6/prodata/1/aa/6B.COMB.pep.\*  
5: /cgn2\_6/prodata/1/aa/PCFUS.COMB.pep.\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	5	4	US-10-015-328-8
2	26	100.0	5	4	US-09-728-653-8
3	20	76.9	4	4	US-10-015-328-9
4	20	76.9	4	4	US-10-015-328-10
5	20	76.9	4	4	US-09-728-653-9
6	20	76.9	4	4	US-09-728-653-10
7	17	65.4	5	3	US-09-020-880-41
8	17	65.4	5	3	US-09-101-544-41
9	16	61.5	4	1	US-08-335-198-21
10	16	61.5	5	3	US-09-357-952-68
11	16	61.5	5	3	US-09-521-650-68
12	16	61.5	5	3	US-09-168-888-68
13	16	61.5	5	4	US-09-947-387-68
14	16	61.5	5	4	US-09-368-670C-10
15	16	61.5	5	4	US-09-368-670C-34
16	15	57.7	4	1	US-08-384-618-2
17	15	57.7	4	1	US-08-446-925-9
18	15	57.7	4	1	US-08-456-424-49
19	15	57.7	4	2	US-08-800-007A-10
20	15	57.7	4	2	US-09-146-331-9
21	15	57.7	4	2	US-08-814-577-2
22	15	57.7	4	2	US-08-915-414A-1
23	15	57.7	4	2	US-08-896-885-9
24	15	57.7	4	2	US-08-712-878-2
25	15	57.7	4	3	US-09-226-568-39
26	15	57.7	4	3	US-08-802-981-2
27	15	57.7	4	3	US-08-802-981-3

28	15	57.7	4	3	US-08-802-981-177	Sequence 177, App
29	15	57.7	4	3	US-09-039-308A-15	Sequence 15, Appl
30	15	57.7	4	3	US-09-039-308A-17	Sequence 17, Appl
31	15	57.7	4	3	US-09-270-735-2	Sequence 2, Appl
32	15	57.7	4	3	US-09-167-921-42	Sequence 42, Appl
33	15	57.7	4	3	US-09-270-736-1	Sequence 1, Appl
34	15	57.7	4	3	US-08-973-462-29	Sequence 29, Appl
35	15	57.7	4	3	US-08-761-483-3	Sequence 3, Appl
36	15	57.7	4	3	US-08-761-483-10	Sequence 10, Appl
37	15	57.7	4	3	US-09-323-743-42	Sequence 42, Appl
38	15	57.7	4	3	US-09-058-969-2	Sequence 2, Appl
39	15	57.7	4	3	US-09-130-193-1	Sequence 1, Appl
40	15	57.7	4	3	US-09-130-193-7	Sequence 7, Appl
41	15	57.7	4	3	US-09-130-193-12	Sequence 12, Appl
42	15	57.7	4	3	US-09-130-193-15	Sequence 15, Appl
43	15	57.7	4	3	US-09-357-952-5	Sequence 5, Appl
44	15	57.7	4	3	US-09-309-003-1	Sequence 1, Appl
45	15	57.7	4	3	US/08/869	Sequence 1, Appl

## ALIGNMENTS

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RESULT 1
US-10-015-328-8
; Sequence 8, Application US/10015328
; Patent No. 6727366
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-10-015-328-8
Query Match 100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVP 5
DB 1 DEVP 5
RESULT 2
US-09-728-653-8
; Sequence 8, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi

```

APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease  
FILE REFERENCE: PH-7118  
CURRENT APPLICATION NUMBER: US/09/728,653  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 60/168,998  
PRIOR FILING DATE: 1999-12-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (2)..(2)  
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl  
US-09-728-653-8

Query Match 100.0%; Score 26; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
Db 1 DEVP 5

RESULT 3  
US-10-015-328-9  
Sequence 9, Application US/10015328  
Patent No. 6727366  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus  
FILE REFERENCE: PH-7203  
CURRENT APPLICATION NUMBER: US/10/015,328  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 60/255,168  
PRIOR FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: N-terminal Protecting Group: benzyloxycarbonyl  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (4)..(4)  
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl  
US-10-015-328-9

Query Match 76.9%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
Db 1 EVVP 4

RESULT 4  
US-10-015-328-10  
Sequence 10, Application US/10015328  
Patent No. 6727366  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus  
FILE REFERENCE: PH-7203  
CURRENT APPLICATION NUMBER: US/10/015,328  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 60/255,168  
PRIOR FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl  
US-10-015-328-10

Query Match 76.9%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
Db 1 EVVP 4

RESULT 5  
US-09-728-653-9  
Sequence 9, Application US/09728653  
Patent No. 6774212  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease  
FILE REFERENCE: PH-7118  
CURRENT APPLICATION NUMBER: US/09/728,653  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 60/168,998  
PRIOR FILING DATE: 1999-12-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: N-terminal Protecting Group: benzyloxycarbonyl  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (4)..(4)



OTHER INFORMATION: Benzyl Esterification  
US-09-728-653-9

Query Match 76.9%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
DB 1 EVVP 4

RESULT 6  
US-09-728-653-10  
Sequence 10, Application US/09728653  
Patent No. 6774212

GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease  
FILE REFERENCE: PH-7118  
CURRENT APPLICATION NUMBER: US/09/728,653  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 60/168,998  
PRIOR FILING DATE: 1999-12-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MOD RES  
LOCATION: (1)-(1)  
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl  
US-09-728-653-10

Query Match 76.9%; Score 20; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
DB 1 EVVP 4

RESULT 7  
US-09-020-880-41  
Sequence 41, Application US/09020880A  
Patent No. 6136558  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ballinger, Marcus D.  
APPLICANT: Jones, Jennifer T.  
APPLICANT: Fairbrother, Wayne J.  
APPLICANT: Sliwowski, Mark X.  
APPLICANT: Wells, James A.  
TITLE OF INVENTION: HEREGULIN VARIANTS  
FILE REFERENCE: 14918-720CON1  
CURRENT APPLICATION NUMBER: US/09/020,880A  
CURRENT FILING DATE: 1998-02-09  
EARLIER APPLICATION NUMBER: US 60/037,581  
PRIOR FILING DATE: 1997-02-10  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 41  
LENGTH: 5  
TYPE: PRT  
ORGANISM: No. 6136558 relevant (recombinant)  
US-09-020-880-41

Query Match 65.4%; Score 17; DB 3; Length 5;  
Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
DB 2 EVVP 5

RESULT 8  
US-09-101-544-41  
Sequence 41, Application US/09101544  
Patent No. 6387638

GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ballinger, Marcus D.  
APPLICANT: Jones, Jennifer T.  
APPLICANT: Fairbrother, Wayne J.  
APPLICANT: Sliwowski, Mark X.  
APPLICANT: Wells, James A.  
TITLE OF INVENTION: HEREGULIN VARIANTS  
FILE REFERENCE: 14918-720CON2  
CURRENT APPLICATION NUMBER: US/09/101,544  
CURRENT FILING DATE: 1998-07-17  
PRIOR APPLICATION NUMBER: US 09/020,880  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: US 60/037,581  
PRIOR FILING DATE: 1997-02-10  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 41  
LENGTH: 5  
TYPE: PRT  
ORGANISM: No. 6387638 relevant (recombinant)  
US-09-101-544-41

Query Match 65.4%; Score 17; DB 3; Length 5;  
Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
DB 2 EVVP 5

RESULT 9  
US-08-335-198-21  
Sequence 21, Application US/08335198  
Patent No. 5637454  
GENERAL INFORMATION:  
APPLICANT: Harley, John B.  
TITLE OF INVENTION: Assays and Treatments for Autoimmune  
TITLE OF INVENTION: Diseases  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Ste. 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30309-4539  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,198  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/648205

FILING DATE: 01-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF 114CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 815-6508  
TELEFAX: (404) 815-6555  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-335-198-21

Query Match 61.5%; Score 16; DB 1; Length 4;  
Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 4  
DB 1 DEVP 4

RESULT 10  
US-09-357-952-68  
Sequence 68, Application US/09357952  
GENERAL INFORMATION:  
APPLICANT: Zhang, Han-Zhong  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Drewe, John A.  
TITLE OF INVENTION: No. 6248904e1 Fluorescence Dyes and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases, Peptidases, Proteases  
TITLE OF INVENTION: Other Enzymes and the Use Thereof  
FILE REFERENCE: 1735.0030001  
CURRENT FILING DATE: 1999-07-21  
EARLIER FILING DATE: 1999-07-21  
EARLIER APPLICATION NUMBER: US 60/093,642  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 68  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-357-952-68

Query Match 61.5%; Score 16; DB 3; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYVP 5  
DB 1 DIVP 4

RESULT 11  
US-09-521-650-68  
Sequence 68, Application US/09521650  
Patent No. 6335429  
GENERAL INFORMATION:

APPLICANT: Weber, Eckard  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Keana, John F.W.  
APPLICANT: Drewe, John A.  
APPLICANT: Zhang, Han-Zhong  
TITLE OF INVENTION: No. 6335429e1 Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof  
FILE REFERENCE: 1735.0290002  
CURRENT APPLICATION NUMBER: US/09/521,650  
CURRENT FILING DATE: 2000-03-08  
EARLIER APPLICATION NUMBER: 09/168,888  
EARLIER FILING DATE: 1998-10-09  
EARLIER APPLICATION NUMBER: US 60/061,582  
EARLIER FILING DATE: 1997-10-10  
EARLIER APPLICATION NUMBER: US 09/033,661  
EARLIER FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 68  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-521-650-68

Query Match 61.5%; Score 16; DB 3; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYVP 5  
DB 1 DIVP 4

RESULT 12  
US-09-168-888-68  
Sequence 68, Application US/09168888  
Patent No. 6342611  
GENERAL INFORMATION:  
APPLICANT: Weber, Eckard  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Keana, John F.W.  
APPLICANT: Zhang, Han-Zhong  
TITLE OF INVENTION: No. 6342611e1 Fluorescent Reporter Molecules and Their Applications for Whole-Cell Fluorescence Screening Assays for Caspases and Other Enzymes and the Use Thereof  
FILE REFERENCE: 1735.0290002  
CURRENT APPLICATION NUMBER: US/09/168,888  
CURRENT FILING DATE: 1998-10-09  
EARLIER APPLICATION NUMBER: US 60/061,582  
EARLIER FILING DATE: 1997-10-10  
EARLIER APPLICATION NUMBER: US 09/033,661  
EARLIER FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 68  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-168-888-68

Query Match 61.5%; Score 16; DB 3; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
: : :  
Db 1 DIVP 4

## RESULT 13

US-09-947-387-68  
; Sequence 68, Application US/09947387  
; Patent No. 6759207  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. 6759207e1 Fluorogenic or Fluorescent Reporter Molecules and  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290005  
; CURRENT APPLICATION NUMBER: US/09/947,387  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 68  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; US-09-947-387-68

Query Match 61.5%; Score 16; DB 4; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
: : :  
Db 1 DIVP 4

## RESULT 14

US-09-368-670C-10  
; Sequence 10, Application US/09368670C  
; Patent No. 6767991  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.  
; TITLE OF INVENTION: Hepatitis C Inhibitor Peptides  
; FILE REFERENCE: 13/063-2-C2  
; CURRENT APPLICATION NUMBER: US/09/368,670C  
; CURRENT FILING DATE: 1999-08-05  
; PRIOR APPLICATION NUMBER: 60/095,945  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/055,186  
; PRIOR FILING DATE: 1997-08-11  
; PRIOR APPLICATION NUMBER: 09/131,758  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Hepatitis C  
; FEATURE:  
; NAME/KEY: VARIANT

; LOCATION: 1  
; OTHER INFORMATION: Asp is capped with DAD  
; US-09-368-670C-10

Query Match 61.5%; Score 16; DB 4; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
: : :  
Db 1 DIVP 4

## RESULT 15

US-09-368-670C-34  
; Sequence 34, Application US/09368670C  
; Patent No. 6767991  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.  
; TITLE OF INVENTION: Hepatitis C Inhibitor Peptides  
; FILE REFERENCE: 13/063-2-C2  
; CURRENT APPLICATION NUMBER: US/09/368,670C  
; CURRENT FILING DATE: 1999-08-05  
; PRIOR APPLICATION NUMBER: 60/095,945  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/055,186  
; PRIOR FILING DATE: 1997-08-11  
; PRIOR APPLICATION NUMBER: 09/131,758  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Hepatitis C  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 5  
; OTHER INFORMATION: Xaa=Nva  
; NAME/KEY: VARIANT  
; LOCATION: 1  
; OTHER INFORMATION: Asp is capped with DAD  
; US-09-368-670C-34

Query Match 61.5%; Score 16; DB 4; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
: : :  
Db 1 DIVP 4

Search completed: December 8, 2004, 08:34:19  
Job time : 38 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 08:30:16 ; Search time 852 Seconds  
(without alignments)  
2.096 Million cell updates/sec

Title: SRQ1  
Sequence: 1 decomp 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 20731

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

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- 2: /cgn2\_6/prodata/1/pubppa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*
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- 10: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/prodata/1/pubppa/US10\_PUBCOMB.pep:\*
- 17: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/prodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	5	US-09-728-653-8	Sequence 8, Appli
2	26	100.0	5	US-10-015-328-8	Sequence 8, Appli
3	20	76.9	4	US-09-728-653-9	Sequence 9, Appli
4	20	76.9	4	US-09-728-653-10	Sequence 10, Appli
5	20	76.9	4	US-10-015-328-9	Sequence 10, Appli
6	20	76.9	4	US-10-015-328-10	Sequence 10, Appli
7	17	65.4	5	US-10-082-747A-41	Sequence 41, Appli
8	16	61.5	5	US-09-777-785-2	Sequence 2, Appli
9	16	61.5	5	US-09-777-785-4	Sequence 4, Appli
10	16	61.5	5	US-09-777-785-5	Sequence 5, Appli
11	16	61.5	5	US-09-777-785-6	Sequence 6, Appli
12	16	61.5	5	US-09-947-387-68	Sequence 68, Appli
13	16	61.5	5	US-10-138-375-68	Sequence 68, Appli

14	16	61.5	5	17	US-10-829-381-68	Sequence 68, Appli
15	15	57.7	4	8	US-08-865-579-81	Sequence 81, Appli
16	15	57.7	4	8	US-08-865-579-82	Sequence 82, Appli
17	15	57.7	4	9	US-09-045-620-4	Sequence 4, Appli
18	15	57.7	4	9	US-09-734-846-42	Sequence 42, Appli
19	15	57.7	4	9	US-09-746-731-81	Sequence 81, Appli
20	15	57.7	4	9	US-09-746-731-82	Sequence 82, Appli
21	15	57.7	4	9	US-09-799-463-2	Sequence 2, Appli
22	15	57.7	4	9	US-09-735-363A-85	Sequence 85, Appli
23	15	57.7	4	9	US-09-799-994-2	Sequence 2, Appli
24	15	57.7	4	9	US-09-745-204-2	Sequence 2, Appli
25	15	57.7	4	9	US-09-780-142-3	Sequence 71, Appli
26	15	57.7	4	9	US-09-765-105-2	Sequence 2, Appli
27	15	57.7	4	9	US-09-858-754-6	Sequence 6, Appli
28	15	57.7	4	9	US-09-858-754-11	Sequence 11, Appli
29	15	57.7	4	9	US-09-858-754-11	Sequence 3, Appli
30	15	57.7	4	9	US-09-987-417-3	Sequence 2, Appli
31	15	57.7	4	9	US-09-863-649-2	Sequence 1, Appli
32	15	57.7	4	9	US-09-737-255-1	Sequence 1, Appli
33	15	57.7	4	9	US-09-920-332-1	Sequence 8, Appli
34	15	57.7	4	9	US-09-845-028-8	Sequence 52, Appli
35	15	57.7	4	9	US-09-954-687-52	Sequence 9, Appli
36	15	57.7	4	9	US-09-270-983-9	Sequence 5, Appli
37	15	57.7	4	9	US-09-947-387-5	Sequence 29, Appli
38	15	57.7	4	9	US-09-742-096-29	Sequence 1, Appli
39	15	57.7	4	10	US-09-819-266-1	Sequence 2, Appli
40	15	57.7	4	10	US-09-161-172-2	Sequence 7, Appli
41	15	57.7	4	10	US-09-866-512A-7	Sequence 1, Appli
42	15	57.7	4	10	US-09-862-224-1	Sequence 6, Appli
43	15	57.7	4	13	US-10-103-448-6	Sequence 3, Appli
44	15	57.7	4	13	US-10-099-408A-3	Sequence 3, Appli
45	15	57.7	4	13	US-10-059-749-81	Sequence 81, Appli

#### ALIGNMENTS

RESULT 1  
US-09-728-653-8  
; Sequence 8, Application US/09728653  
; Publication No. US20020123468A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Alpha-Ketocamide Inhibitors of Hepatitis C Virus NS3 Protease  
FILE REFERENCE: PH-7118  
CURRENT APPLICATION NUMBER: US/09/728,653  
CURRENT FILING DATE: 2000-12-01  
PRIORITY APPLICATION NUMBER: US 60/166,998  
PRIORITY FILING DATE: 1999-12-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MOD RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl  
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (2)..(2)  
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl  
US-09-728-653-8  
Query Match 100.0%; Score 26; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
Db 1 DEVP 5

## RESULT 2

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US-10-015-328-8
; Sequence 8, Application US/10015328
; Publication No. US20030100768A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (2)-(2)
; OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
US-10-015-328-8

```

Query Match 100.0%; Score 26; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
Db 1 DEVP 5

## RESULT 3

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US-09-728-653-9
; Sequence 9, Application US/09728653
; Publication No. US20020123468A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD_RES

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; LOCATION: (1)-(1)
; OTHER INFORMATION: N-terminal Protecting Group: benzyloxycarbonyl
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)-(4)
; OTHER INFORMATION: Benzyl Esterification
US-09-728-653-9

```

Query Match 76.9%; Score 20; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYVP 5  
Db 1 EYVP 4

## RESULT 4

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US-09-728-653-10
; Sequence 10, Application US/09728653
; Publication No. US20020123468A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-09-728-653-10

```

Query Match 76.9%; Score 20; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYVP 5  
Db 1 EYVP 4

## RESULT 5

```

US-10-015-328-9
; Sequence 9, Application US/10015328
; Publication No. US20030100768A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9

```

```

; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: benzylloxycarbonyl
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Benzyl Esterification
US-10-015-328-9

Query Match
Best Local Similarity 100.0%; Score 20; DB 14; Length 4;
Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
   |||
Db 1 EVVP 4

RESULT 6
US-10-015-328-10
; Sequence 10, Application US/10015328
; Publication No. US20030100768A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Q1
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Vir
; TITLE OF INVENTION: Protease Inhibitors
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-10-015-328-10

Query Match
Best Local Similarity 76.9%; Score 20; DB 14; Length 4;
Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
   |||
Db 1 EVVP 4

RESULT 7
US-10-082-747A-41
; Sequence 41, Application US/10082747A
; Publication No. US20030129688A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Slikowski, Mark X.
```

```

; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HEREGULIN VARIANTS
; FILE REFERENCE: 402E-4/612US
; CURRENT APPLICATION NUMBER: US/10/082,747A
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/101,544
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PCT/US/98/01579
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 08/799,054
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatsEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant sequence at human heregulin-beta1
; OTHER INFORMATION: residues 177-181
US-10-082-747A-41

Query Match
Best Local Similarity 65.4%; Score 17; DB 14; Length 5;
Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5
   |||
Db 2 EVVP 5

RESULT 8
US-09-777-785-2
; Sequence 2, Application US/09777785
; Patent No. US20020103135A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ramin
; TITLE OF INVENTION: Aza-peptides Useful In The Treatment Of Hepatitis C
; FILE REFERENCE: IN01130K1 US
; CURRENT APPLICATION NUMBER: US/09/777,785
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/181,017
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:azapeptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
; NAME/KEY: UNSURE
; LOCATION: (5)
; OTHER INFORMATION: 2-[(4-nitrophenoxy)carbonyl]-2-propylhydrazine
; NAME/KEY: UNSURE
; LOCATION: (2)
; OTHER INFORMATION: Xaa=D-gamma-carboxyglutamic acid
US-09-777-785-2

Query Match
Best Local Similarity 61.5%; Score 16; DB 9; Length 5;
Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEVP 5
   |||
Db 1 EVVP 5

RESULT 9
US-09-777-785-4
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/ Sequence 4, Application US/09777785
/ Patent No. US20020103135A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Rumin
/ TITLE OF INVENTION: Azapeptides Useful In The Treatment Of Hepatitis C
/ FILE REFERENCE: IN01130X1 US
/ CURRENT APPLICATION NUMBER: US/09/777,785
/ PRIOR FILING DATE: 2001-02-06
/ PRIOR APPLICATION NUMBER: 60/181,017
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:azapeptide
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: UNSURE
/ LOCATION: (5)
/ OTHER INFORMATION: 2-[(1-chloro-2-methylpropyloxy)carbonyl]-2-propylhy
/ OTHER INFORMATION: ydrazine
/ NAME/KEY: UNSURE
/ LOCATION: (2)
/ OTHER INFORMATION: Xaa=D-gamma-carboxyglutamic acid
US-09-777-785-4
```

```
Query Match      61.5%; Score 16; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 DEVP 5
       : |||
Db      1 EXVVP 5
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RESULT 10
US-09-777-785-5
/ Sequence 5, Application US/09777785
/ Patent No. US20020103135A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Rumin
/ TITLE OF INVENTION: Azapeptides Useful In The Treatment Of Hepatitis C
/ FILE REFERENCE: IN01130X1 US
/ CURRENT APPLICATION NUMBER: US/09/777,785
/ PRIOR FILING DATE: 2001-02-06
/ PRIOR APPLICATION NUMBER: 60/181,017
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:azapeptide
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: UNSURE
/ LOCATION: (5)
/ OTHER INFORMATION: 2-[(chloromethoxy)carbonyl]-2-propylhydrazine
/ NAME/KEY: UNSURE
/ LOCATION: (2)
/ OTHER INFORMATION: Xaa=D-gamma-carboxyglutamic acid
US-09-777-785-5
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```
Query Match      61.5%; Score 16; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 DEVP 5
       : |||
Db      1 EXVVP 5
```

```
RESULT 11
US-09-777-785-6
/ Sequence 6, Application US/09777785
/ Patent No. US20020103135A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Rumin
/ TITLE OF INVENTION: Azapeptides Useful In The Treatment Of Hepatitis C
/ FILE REFERENCE: IN01130X1 US
/ CURRENT APPLICATION NUMBER: US/09/777,785
/ PRIOR FILING DATE: 2001-02-06
/ PRIOR APPLICATION NUMBER: 60/181,017
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:azapeptide
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: UNSURE
/ LOCATION: (5)
/ OTHER INFORMATION: 2-[(1,2,2,2-tetrachloroethoxy)carbonyl]-2-propylhy
/ OTHER INFORMATION: drazine
/ NAME/KEY: UNSURE
/ LOCATION: (2)
/ OTHER INFORMATION: Xaa=D-gamma-carboxyglutamic acid
US-09-777-785-6
```

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Query Match      61.5%; Score 16; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 DEVP 5
       : |||
Db      1 EXVVP 5
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```
RESULT 12
US-09-947-387-68
/ Sequence 68, Application US/09947387
/ Patent No. US20020150885A1
/ GENERAL INFORMATION:
/ APPLICANT: Weber, Eckard
/ APPLICANT: Cai, Sui Xiong
/ APPLICANT: Keana, John F.W.
/ APPLICANT: Drewe, John A.
/ APPLICANT: Zhang, Han-Zhong
/ TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecule
/ TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
/ TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
/ FILE REFERENCE: 1735.0290005
/ CURRENT APPLICATION NUMBER: US/09/947,387
/ PRIOR FILING DATE: 2001-09-07
/ PRIOR APPLICATION NUMBER: US 60/061,582
/ PRIOR FILING DATE: 1997-10-10
/ PRIOR APPLICATION NUMBER: US 60/145,746
/ PRIOR FILING DATE: 1998-03-03
/ PRIOR APPLICATION NUMBER: US 09/168,888
/ NUMBER OF SEQ ID NOS: 142
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 68
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LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
OTHER INFORMATION: Peptide  
US-09-947-387-68

Query Match 61.5%; Score 16; DB 9; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
Db 1 DIVP 4

RESULT 13  
US-10-138-375-68  
Sequence 68, Application US/10138375  
Publication No. US20030208037A1  
GENERAL INFORMATION:  
APPLICANT: Zhang, Han-Zhong  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Drewe, John A.  
APPLICANT: Yang, Wu  
TITLE OF INVENTION: No. US20030208037A1 Fluorescence Dyes and Their Applications for  
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
TITLE OF INVENTION: Other Enzymes and the Use Thereof  
FILE REFERENCE: 1735-0030001  
CURRENT APPLICATION NUMBER: US/10/138,375  
PRIORITY FILING DATE: 2002-05-06  
PRIORITY FILING DATE: EARLIER APPLICATION NUMBER: US/09/357,952  
PRIORITY FILING DATE: EARLIER FILING DATE: 1999-07-21  
PRIORITY FILING DATE: EARLIER APPLICATION NUMBER: US 60/093,642  
PRIORITY FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 68  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
OTHER INFORMATION: Peptide  
US-10-138-375-68

Query Match 61.5%; Score 16; DB 14; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
Db 1 DIVP 4

RESULT 14  
US-10-829-381-68  
Sequence 68, Application US/10829381  
Publication No. US20040191844A1  
GENERAL INFORMATION:  
APPLICANT: Weber, Eckard  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Keana, John F.W.  
APPLICANT: Drewe, John A.  
APPLICANT: Zhang, Han-Zhong  
TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and  
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
TITLE OF INVENTION: Use Thereof  
FILE REFERENCE: 1735-0290006  
CURRENT APPLICATION NUMBER: US/10/829,381  
CURRENT FILING DATE: 2004-04-22

PRIOR APPLICATION NUMBER: US 60/061,582  
PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: US 60/145,746  
PRIOR FILING DATE: 1998-03-03  
PRIOR APPLICATION NUMBER: US 09/168,888  
PRIOR FILING DATE: 1998-10-09  
PRIOR APPLICATION NUMBER: US 09/947,387  
PRIOR FILING DATE: 2001-09-07  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 68  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
OTHER INFORMATION: Peptide  
US-10-829-381-68

Query Match 61.5%; Score 16; DB 17; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVVP 5  
Db 1 DIVP 4

RESULT 15  
US-08-865-579-81  
Sequence 81, Application US/08865579  
Publication No. US20010006779A1  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
TITLE OF INVENTION: Encoding Same and Methods of Use  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
City: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/865,579  
FILING DATE: 29-MAY-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 2180  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-9849  
INFORMATION FOR SEQ ID NO: 81:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 4  
OTHER INFORMATION: /note="Amino Acid is bonded to an  
OTHER INFORMATION: aldehyde at the C-terminal."

US-08-865-579-81

Query Match

Best Local Similarity 57.7%; Score 15; DB 8; Length 4;

Matches 3; Conservatave 0; Mismatches 0; Indels 0;

QY 1 DEV 3

Db 1 DEV 3

Search completed: December 8, 2004, 08:48:38  
Job time : 853 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 08:30:15 ; Search time 38 Seconds  
(without alignments)  
12.660 Million cell updates/sec

Title: SEQ1  
Perfect score: 26  
Sequence: 1 devvp 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Match Length	DB	ID	Description
1	46.2	4	2	A61300	22K superhelical D
2	42.3	4	2	I54357	Schwannomin - mous
3	42.3	4	2	S17255	ribosomal protein
4	42.3	5	2	B22565	R-phycocerythrin al
5	42.3	5	2	PT0281	Ig heavy chain CRD
6	42.3	5	2	PT0656	T-cell receptor be
7	42.3	5	2	PT0573	T-cell receptor be
8	42.3	5	2	A60521	glycogen phosphory
9	42.3	5	2	A32014	tram protein - Bsc
10	34.6	5	2	A44692	fulicin - giant Af
11	30.8	3	3	I78890	tyrosine protein k
12	30.8	4	1	I40697	bioerin A - Clitroba
13	30.8	4	1	H0R0HA	proctolin - Americ
14	30.8	5	2	JN0860	peptidyl-dipeptida
15	30.8	5	2	S53595	hypothetical prote
16	30.8	5	2	PT0679	T-cell receptor de
17	30.8	5	2	E42364	flagellar protein
18	30.8	5	2	A60411	proctolin - Atlant
19	30.8	5	2	PT0601	T-cell receptor be
20	26.9	3	3	RHSHT	thryoliberin - she
21	26.9	3	3	A92971	thryoliberin - eas
22	26.9	3	3	RHTDPO	thryoliberin - Bom
23	26.9	3	3	A43391	trh-like tripeptid
24	26.9	3	3	RHPT	thryoliberin - pig
25	26.9	3	3	A33802	phagocytosis-stimu
26	26.9	4	2	A02147	scarvation-induced
27	26.9	4	2	S53508	glucan 1,4-alpha-g
28	26.9	4	2	A27897	RPCH-related neuro
29	26.9	4	2	A34626	

30	7	26.9	4	2	I51049	metallothionein-A
31	7	26.9	4	2	PT0240	Ig heavy chain CRD
32	7	26.9	4	2	S55238	pallidipin - assa
33	7	26.9	4	2	PL0140	carbon-monoxide de
34	7	26.9	4	2	PT0271	Ig heavy chain CRD
35	7	26.9	4	2	PT0675	T-cell receptor be
36	7	26.9	4	2	A32039	tyrosine-melanocyt
37	7	26.9	5	2	JN0862	peptidyl-dipeptida
38	7	26.9	5	2	C41225	copper resistance
39	7	26.9	5	2	A41225	copper resistance
40	7	26.9	5	2	B60274	major protein anti
41	7	26.9	5	2	E60274	major protein anti
42	7	26.9	5	2	P00009	angiotensin-conver
43	7	26.9	5	2	P00689	photosystem I 10.4
44	7	26.9	5	2	PS0324	ribulose-bisphosph
45	7	26.9	5	2	B37988	acid proteinase 11

## ALIGNMENTS

RESULT 1  
A61300  
22K superhelical DNA-binding protein - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C:Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C:Accession: A61300  
R:Kishi, F.; Ebina, Y.; Miyai, T.; Nakazawa, T.; Nakazawa, A.  
J. Biochem. 92, 1059-1068, 1982  
A:Title: Purification and characterization of a protein from Escherichia coli which forms  
A:Reference number: A61300; MUID:83082696; PMID:6294066  
A:Accession: A61300  
A:Molecule type: protein  
A:Residues: 1-4 <KIS>  
A:Comment: This protein resembles some of the histone-like protein of bacteria in amino  
C:Keywords: DNA binding; monomer

Query Match  
Best Local Similarity 46.2%; Score 12; DB 2; Length 4;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVV 4  
DB 2 EIV 4

RESULT 2  
I54357  
Schwannomin - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I54357  
R:Huyh, D.P.; Nechiporuk, T.; Puls, S.  
Hum Mol Genet. 3, 1075-1079, 1994  
A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co  
A:Reference number: I54357; MUID:95072570; PMID:7981675  
A:Accession: I54357  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-4 <RSG>  
A:Cross-references: GB:I28038; NID:G454836; PIDN:AAA57150.1; PID:9601923  
C:Genetics:  
A:Gene: NF2

Query Match  
Best Local Similarity 42.3%; Score 11; DB 2; Length 4;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5  
DB 1 VP 2

RESULT 3  
S17255  
ribosomal protein Yml1, mitochondrial, questionable - Yeast (Saccharomyces cerevisiae)  
C/Species: Saccharomyces cerevisiae  
A/Variety: strain 07173  
C/Date: 23-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 09-Jul-2004  
C/Accession: S17255  
R/Grohmann, L.; Graak, H.R.; Kruf, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.  
A/Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from  
A/Reference number: S17255; MUID:91265106; PMID:2060626  
A/Accession: S17255  
A/Molecule type: protein  
A/Residues: 1-4 <GRO>  
A/Cross-references: UNIPROT:P36515  
C/Comment: A coding region for this protein could not be identified in the genome of Sac  
C/Genetics:  
A/Genome: nuclear  
C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 42.3%; Score 11; DB 2; Length 4;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 VVP 5  
DB 2 VVP 4

RESULT 4  
B22565  
R-phycoerythrin alpha-2 chain - red alga (Gastrocionium coulteri) (fragment)  
C/Species: Gastrocionium coulteri  
C/Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C/Accession: B22565  
R/Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A/Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A/Reference number: A22565; MUID:85182601; PMID:3886644  
A/Accession: B22565  
A/Molecule type: protein  
A/Residues: 1-5 <KLO>

Query Match 42.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VP 5  
DB 3 VP 4

RESULT 5  
PT0281

Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0281

R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0281  
A/Molecule type: DNA  
A/Residues: 1-5 <YAM>  
A/Experimental source: B lymphocyte  
C/Keywords: heterotetramer; immunoglobulin

Query Match 42.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DE 2

DB 1 DE 2

RESULT 6  
PT0656  
T-cell receptor beta chain V-D-J region (121-107) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PT0656  
R/Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A/Reference number: PT0509; MUID:91277601; PMID:1711558  
A/Accession: PT0656  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-5 <FEE>  
A/Experimental source: day 4 postnatal thymus, strain BALB/c  
C/Keywords: T-cell receptor

Query Match 42.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DE 2  
DB 4 DE 5

RESULT 7  
PT0573  
T-cell receptor beta chain V-D-J region (141-100) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PT0573  
R/Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A/Reference number: PT0509; MUID:91277601; PMID:1711558  
A/Accession: PT0573  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-5 <FEE>  
A/Experimental source: day 19 fetal thymus, strain BALB/c  
C/Keywords: T-cell receptor

Query Match 42.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DE 2  
DB 4 DE 5

RESULT 8  
A60521

glycogen phosphorylase (BC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)  
N/Alternate names: glycogen phosphorylase b  
C/Species: Liza ramada  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 15-Mar-2004  
C/Accession: A60521  
R/Bonamura, L.; Baanante, I.V.  
Comp. Biochem. Physiol. B 95, 295-301, 1990  
A/Title: Purification and characterization of glycogen phosphorylase B from skeletal musc  
A/Reference number: A60521; MUID:90227907; PMID:2109669  
A/Accession: A60521  
A/Molecule type: protein  
A/Residues: 1-5 <BON>

C/Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein  
F/3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experime

Query Match 42.3%; Score 11; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5  
 ||  
 DB 4 VP 5

## RESULT 9

A32014  
 t3am protein - Escherichia coli plasmid R100 (fragment)  
 C:Species: Escherichia coli  
 C>Date: 22-Jun-1989 #sequence\_revision 22-Jun-1989 #text\_change 09-Jul-2004  
 C:Accession: A32014  
 R:Inamoto, S.; Yoshioke, Y.; Ohtsubo, E.  
 J. Bacteriol. 170, 2749-2757, 1988  
 A>Title: Identification and characterization of the products from the traJ and traY genes  
 A:Reference number: A32014; MUID:88227859; PMID:2836369  
 A:Accession: A32014  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-5 <DNA>  
 A:Cross-references: UNIPROT:P13973  
 C:Genetics:  
 A:Genome: plasmid  
 C:Keywords: DNA binding

Query Match 42.3%; Score 11; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2  
 ||  
 DB 3 DE 4

## RESULT 10

A44692  
 fulicin - giant African snail  
 C:Species: Achatina fulica (giant African snail)  
 C>Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
 C:Accession: A44692  
 R:Ohba, N.; Kubota, I.; Takeo, T.; Shimomishi, Y.; Yaenda-Kamatani, Y.; Minakata, H.; No  
 Biochem. Biophys. Res. Commun. 178, 486-493, 1991  
 A>Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t  
 A:Reference number: A44692; MUID:91315471; PMID:1859408  
 A:Accession: A44692  
 A:Molecule type: protein  
 A:Residues: 1-5 <OH>  
 A:Cross-references: UNIPROT:P35905  
 C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide  
 P:2/Modified site: D-asparagine (Asn) #status experimental  
 F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 34.6%; Score 9; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DE 4  
 ||  
 DB 2 NEFV 5

## RESULT 11

I78890  
 tyrosine protein kinase - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: I78890  
 R:Chow, L.W.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Luy, M.S.; Kozak, C.  
 Oncogene 9, 3437-3448, 1994  
 A>Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protei

A:Reference number: 158407; MUID:95060800; PMID:7970703

A:Accession: I78890  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3 <RES>  
 A:Cross-references: GB:I33339; NID:5609536; PID:AAA64432.1; PID:9609538  
 C:Genetics:  
 A:Gene: p52ntk

Query Match 30.8%; Score 8; DB 3; Length 3;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5  
 ||  
 DB 1 MP 2

## RESULT 12

I10697  
 biotin A - Citrobacter freundii (fragment)  
 C:Species: Citrobacter freundii  
 C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: I10697  
 R:Shuan, D.; Campbell, A.  
 Gene 67, 203-211, 1988  
 A>Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter  
 A:Reference number: I10697; MUID:89006280; PMID:2971595  
 A:Accession: I10697  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-4 <RES>  
 A:Cross-references: UNIPROT:P13071; GB:M21922; NID:9144434

Query Match 30.8%; Score 8; DB 2; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DE 2  
 ||  
 DB 3 DD 4

## RESULT 13

H080HA  
 proctolin - American cockroach  
 C:Species: Periplaneta americana (American cockroach)  
 C>Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 09-Jul-2004  
 C:Accession: A01644  
 R:Staratt, A.N.; Brown, B.E.  
 Life Sci. 17, 1253-1256, 1975  
 A>Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insect  
 A:Reference number: A93048; MUID:76074708; PMID:576  
 A:Accession: A01644  
 A:Molecule type: protein  
 A:Residues: 1-5 <STA>  
 A:Cross-references: UNIPROT:P01373  
 A>Note: The synthetic peptide had the same chromatographic, electrophoretic, and pharma  
 R:O'Shea, M.; Adams, M.E.  
 Science 213, 567-569, 1981  
 A>Title: Pentapeptide (proctolin) associated with an identified neuron.  
 A:Reference number: A94260; MUID:81225865; PMID:6113690  
 A:Contents: annotation; biological source  
 C:Comment: This peptide is found in the lateral white neurons, which occur (in the cock  
 innervate the striated hindgut muscles in insects and stimulate contraction of these m  
 C:Superfamily: proctolin  
 C:Keywords: neuropeptide

Query Match 30.8%; Score 8; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VP 5

Db :|  
3 LP 4

## RESULT 14

JN0860  
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito  
C:Species: Sarda orientalis (striped bonito)  
C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C:Accession: JN0860  
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe  
A:Reference number: JN0859; MUID:94080036; PMID:7764272  
A:Accession: JN0860  
A:Molecule type: Protein  
A:Residues: 1-5 <MAT>  
A:Experimental source: intestine  
C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 30.8%; Score 8; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 VP 5  
:|  
Db 2 LP 3

## RESULT 15

S53595  
hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
C:Accession: S53595  
R:Galkhoven, C.F.; Bouwman, P.R.J.; Snippe, L.; Ab, G.  
Nucleic Acids Res. 22, 5540-5547, 1994  
A:Title: Translational start site multiplicity of the CCAAT/enhancer binding protein alpha  
A:Reference number: S53595; MUID:55140613; PMID:7838705  
A:Accession: S53595  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <CAL>  
A:Cross-references: EMBL:X66844

Query Match 30.8%; Score 8; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 VP 5  
:|  
Db 1 MP 2

Search completed: December 8, 2004, 08:31:02  
Job time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 08:33:45 ; Search time 62 Seconds  
(without alignments)  
46.401 Million cell updates/sec

Title: SEQ1  
Perfect score: 26  
Sequence: 1 devvp 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	26	100.0	027873	027873 methanobact
2	26	100.0	0742T2	0742T2 mycobacteri
3	26	100.0	AA803070	AA803070 mycobacte
4	26	100.0	03XUG8	03XUG8 caenorhabdi
5	26	100.0	08SEPX3	08SEPX3 canis fami
6	26	100.0	077X97	077X97 helicoverpa
7	26	100.0	077M48	077M48 helicoverpa
8	26	100.0	099H26	099H26 helicoverpa
9	26	100.0	08Y5W7	08Y5W7 helicoverpa
10	26	100.0	07RE42	07RE42 cryza sativ
11	26	100.0	BAC98628	BAC98628 cryza sat
12	26	100.0	08EN67	08EN67 caenorhabdi
13	26	100.0	06GB20	06GB20 staphylococ
14	26	100.0	06GJH3	06GJH3 staphylococ
15	26	100.0	08NXZ8	08NXZ8 staphylococ
16	26	100.0	049991	049991 lycopersico
17	26	100.0	099W45	099W45 staphylococ
18	26	100.0	07A785	07A785 staphylococ
19	26	100.0	08HXV3	08HXV3 sagittinus oe
20	26	100.0	08HXV4	08HXV4 macaca sp.
21	26	100.0	08HXV5	08HXV5 pongo pygma
22	26	100.0	08HXV6	08HXV6 gorilla gor
23	26	100.0	08HXV7	08HXV7 pan troglod
24	26	100.0	021175	021175 caenorhabdi
25	26	100.0	032933	032933 mycobacteri
26	26	100.0	09CBT7	09CBT7 mycobacteri
27	26	100.0	093T65	093T65 bruceella su
28	26	100.0	08FT05	08FT05 bruceella su
29	26	100.0	092M97	092M97 rhizobium m
30	26	100.0	08TIV3	08TIV3 bruceella me
31	26	100.0	08FW99	08FW99 bruceella su

32	26	100.0	152	2	08YC25	08YC25 bruceella me
33	26	100.0	153	1	ANF_FELCA	09g1d0 felis silve
34	26	100.0	153	1	ANF_HUMAN	P01160 homo sapien
35	26	100.0	153	2	06TFY3	06TFY3 erwinia amy
36	26	100.0	153	2	AAQ97887	AAQ97887 erwinia a
37	26	100.0	155	2	09RIG1	09RIG1 rattus norv
38	26	100.0	161	2	06LCX4	06LCX4 sus scrofa
39	26	100.0	161	2	098Z21	098Z21 rhizobium 1
40	26	100.0	161	2	AA60467	AA60467 sus scrof
41	26	100.0	169	2	06CPA6	06CPA6 apis mellif
42	26	100.0	169	2	AA820468	AA820468 apis mell
43	26	100.0	170	1	SPRT_YERPE	082n66 yerwinia pe
44	26	100.0	170	2	06D080	06D080 erwinia car
45	26	100.0	176	2	0930U3	0930U3 rhizobium m

## ALIGNMENTS

## RESULT 1

ID 027873 PRELIMINARY; PRT; 42 AA.  
AC 027873;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Hypothetical protein MTH1845.  
GN OrderedLocustNames=MTH1845;  
OS Methanobacterium thermoautotrophicum.  
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=187420;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Delta H;  
RA MEDLINE=96037514; PubMed=9371463;  
RA Smith D.R., Doncette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
RA Jiwani N., Cartusio A., Bush D., Safer H., Patwell D., Prabhakar S.,  
RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
deltaH: functional analysis and comparative genomics.";  
RL J. Bacteriol. 179:7135-7155(1997).  
DR EMBL; AE000937; AAB86311.1; -.  
KW PIR; G69113; G69113.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 42 AA; 4806 MW; E60FC64EAL53E91 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 2

ID 0742T2 PRELIMINARY; PRT; 66 AA.  
AC 0742T2;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=MAP0753c;  
OS Mycobacterium paratuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;  
OC Mycobacterium avium complex (MAC).

OK NCBI\_TaxID=1770;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K10;  
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE017229; AAS03070.1; -  
 DR InterPro: IPR001080; 3Fe4SFeDOXIN.  
 DR PRINTS: PR00352; 3FE4SFeDOXIN.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 66 AA; 7199 MW; F691DE3C4BE6F393 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 DB 37 DEVVP 41

RESULT 3  
 AAS03070 PRELIMINARY; PRT; 66 AA.  
 ID AAS03070;  
 AC AAS03070 (TREMBlrel. 27, Created)  
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN MAP0753C.  
 OS Mycobacterium paratuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1770;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K10;  
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE017229; AAS03070.1; -  
 DR Hypothetical protein.  
 KW SEQUENCE 66 AA; 7199 MW; F691DE3C4BE6F393 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 DB 37 DEVVP 41

RESULT 4  
 Q9XUG8 PRELIMINARY; PRT; 74 AA.  
 ID Q9XUG8;  
 AC Q9XUG8;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Hypothetical protein C43F9.7.  
 GN Name=C43F9.7;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RL Science 282:2012-2018 (1998).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Mortimore B.J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z82262; CAB05150.1; -  
 DR PIR: T19911; T19911  
 DR WormRep: C43F9.7; CE19735.  
 KW Hypothetical protein.  
 SQ SEQUENCE 74 AA; 8436 MW; 1437C36F4B4E9F4 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 DB 30 DEVVP 34

RESULT 5  
 Q8SPX3 PRELIMINARY; PRT; 77 AA.  
 ID Q8SPX3;  
 AC Q8SPX3;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Atrial natriuretic peptide (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Rastogi S., Tiwari N., Mishra S., Sabbah H.N., Gupta R.C.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF484116; AAL92021.1; -  
 DR GO: GO:0005576; Cxetracellular; IEA.  
 DR GO: GO:0005179; F: hormone activity; IEA.  
 DR GO: GO:0005179; P: physiological process; IEA.  
 DR InterPro: IPR002407; Atrial natriuretic peptide.  
 DR InterPro: IPR000663; Natr\_peptide.  
 DR Pfam: PF00212; ANP; 1.  
 DR PRINTS: PR00711; ANATPEPTIDE.  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 77 AA; 8290 MW; 32D36091AB7D752 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 DB 22 DEVVP 26

RESULT 6  
 Q77K97 PRELIMINARY; PRT; 87 AA.  
 ID Q77K97;  
 AC Q77K97;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE P10.  
 OS Helicoverpa armigera nuclear polyhedrosis virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=51313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang C.X., Wu J.C.;



```

RT "Genome structure and the p10 gene of the Helicoverpa armigera
  nucleopolyhedrovirus.";
RL Acta Biochim. Biophys. Sin. 33:179-184(2001).
DR EMBL; AF303045; AAK86274.1; -.
DR InterPro; IPR008702; NPV_P10.
DR Pfam; PF05531; NPV_P10; 1.
SQ SEQUENCE 87 AA; 9331 MW; 30A98644B22293FA CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
   |||||
Db 73 DEVVP 77

RESULT 7
Q77M48 PRELIMINARY; PRT; 87 AA.
AC Q77M48;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE p10.
OS Helicoverpa armigera single nucleocapsid polyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
CX NCBI_TaxID=160266;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang H., Chen X., Vlak J.M., Hu Z.;
RT "Sequence and transcriptional analysis of the p10 gene of Helicoverpa
  armigera single nucleocapsid polyhedrovirus.";
RL Ping Tu Hsueh Pao 17:81-86(2001).
DR EMBL; AF265354; AAK57874.1; -.
DR InterPro; IPR008702; NPV_P10.
DR Pfam; PF05531; NPV_P10; 1.
SQ SEQUENCE 87 AA; 9331 MW; 30A98644B22293FA CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
   |||||
Db 73 DEVVP 77

RESULT 8
Q99H26 PRELIMINARY; PRT; 87 AA.
ID Q99H26;
AC Q99H26;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE p10.
OS Helicoverpa armigera nucleopolyhedrovirus G4.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
CX NCBI_TaxID=148363;
RN [1]
RP SEQUENCE FROM N.A.
RA Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
RT "Sequence analysis of the gp37 gene of Heliothis armigera single-
  nucleocapsid nucleopolyhedrovirus.";
RL Zhongguo Bing Du Xue 15:35-42(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
RT "Sequence analysis of the gp37 gene of Heliothis armigera single-
  nucleocapsid nucleopolyhedrovirus.";
RL Zhongguo Bing Du Xue 15:43-49(2000).

```

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RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21078302; PubMed=11210934;
RA Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;
RT "Nucleotide sequence and transcriptional analysis of a putative basic
  DNA-binding protein of Helicoverpa armigera polyhedrovirus.";
RL Virus Genes 22:113-120(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21064569; PubMed=1125177;
RA Chen X., Ickel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
  Peters S., Zuidema D., Iankhorst R.K., Vlak J.M., Hu Z.;
RT "The sequence of the Helicoverpa armigera single-nucleocapsid
  nucleopolyhedrovirus genome.";
RL J. Gen. Virol. 82:241-257(2001).
DR EMBL; AF271059; AAG53764.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR008702; NPV_P10.
DR Pfam; PF05531; NPV_P10; 1.
SQ SEQUENCE 87 AA; 9331 MW; 30A98644B22293FA CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
   |||||
Db 73 DEVVP 77

RESULT 9
Q8V5W7 PRELIMINARY; PRT; 87 AA.
ID Q8V5W7;
AC Q8V5W7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ORF20.
OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
CX NCBI_TaxID=10468;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21830929; PubMed=11842262;
RA Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F.,
  Presnail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlak J.M.;
RT "Comparative analysis of the complete genome sequences of Helicoverpa
  zea and Helicoverpa armigera single-nucleocapsid
  nucleopolyhedroviruses.";
RL J. Gen. Virol. 83:673-684(2002).
DR EMBL; AF34030; AAD56165.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR008702; NPV_P10.
DR Pfam; PF05531; NPV_P10; 1.
SQ SEQUENCE 87 AA; 9353 MW; 30A98A48B22B9FFA CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5
   |||||
Db 73 DEVVP 77

RESULT 10
Q7E242 PRELIMINARY; PRT; 90 AA.
ID Q7E242;
AC Q7E242;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

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DE Hypochemical protein B101SH11.112.  
 GN Name=B101SH11.112;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 RN NCB1\_TaxID=39947;  
 RP SEQUENCE FROM N.A.  
 RA Sasaki T., Matsumoto T., Katayose Y.,  
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP005123; BAC98628.1; -  
 KW Hypochemical protein.  
 SQ SEQUENCE 90 AA; 9784 MW; F76FADCGA944E184 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 26; DB 2; Length 90;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 |||||  
 DB 85 DEVP 89

RESULT 11  
 ID BAC98628 PRELIMINARY; PRT; 90 AA.  
 AC BAC98628;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypochemical protein B101SH11.112.  
 GN B101SH11.112.  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza; Oryza sativa.  
 RN NCB1\_TaxID=39947;  
 RP SEQUENCE FROM N.A.  
 RA Sasaki T., Matsumoto T., Katayose Y.,  
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP005123; BAC98628.1; -  
 KW Hypochemical protein.  
 SQ SEQUENCE 90 AA; 9784 MW; F76FADCGA944E184 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 26; DB 2; Length 90;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 |||||  
 DB 85 DEVP 89

RESULT 12  
 ID Q86NG7 PRELIMINARY; PRT; 99 AA.  
 AC Q86NG7;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DE Hypochemical protein K03B4.7.  
 GN Name=K03B4.7;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Pelicerinae; Caenorhabditis.  
 RN NCB1\_TaxID=6239;  
 RP SEQUENCE FROM N.A.

RC STRAIN-Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA Wilson R.;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Du Z., Le T.T., Kemp K.;  
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Wilson R.;  
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U55370; AA021423.1; -  
 KW Hypochemical protein.  
 SQ SEQUENCE 99 AA; 11281 MW; AEFCCCB4E8527A5 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 26; DB 2; Length 99;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
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 DB 22 DEVP 26

RESULT 13  
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 AC Q6GBZ0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Stage V sporulation protein G.  
 GN ORFNames=SA50455;  
 OS Staphylococcus aureus subsp. aureus MSSA476.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 RN NCB1\_TaxID=282459;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MSSA476;  
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,  
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,  
 RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,  
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,  
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,  
 RA James K.D., Lennard N., Line A., Mayes R., Mould S., Mungall K.,  
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M.,  
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,  
 RA Spratt B.G., Parkhill J.;  
 RT "Complete genomes of two clinical Staphylococcus aureus strains:  
 RT evidence for the rapid evolution of virulence and drug resistance.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).  
 DR EMBL: BX571857; CAG42230.1; -  
 DR InterPro: IPR007170; SpovG.  
 DR Pfam: PF04026; SpovG; 1.  
 SQ SEQUENCE 100 AA; 11278 MW; 876EC2BC87CF74C CRC64;

Query Match  
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
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 DB 84 DEVP 88

## RESULT 14

OG6JH3 PRELIMINARY; PRT; 100 AA.  
 AC OG6JH3;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Stage V sporulation protein G.  
 GN Name=spovG; ORFNames=SA0499;  
 OS Staphylococcus aureus subsp. aureus MRSA252.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=282458;  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN=MRSA252;  
 RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,  
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,  
 RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,  
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,  
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,  
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,  
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K., Sanders M.,  
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,  
 RA Spratt B.G., Parkhill J.;  
 RT "Complete genomes of two clinical Staphylococcus aureus strains:  
 RT evidence for the rapid evolution of virulence and drug resistance.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).  
 DR EMBL; BX571856; CAG39521.1; -;  
 DR InterPro; IPR007170; SpovG.  
 DR Pfam; PF04026; SpovG; 1.  
 SQ SEQUENCE 100 AA; 11290 MW; 877B186C87CF7F4C CRC64;

## Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 100;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 84 DEVP 88

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 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE SpovG protein.  
 GN Name=spovG; OrderedLocusNames=MW0453;  
 OS Staphylococcus aureus (strain MW2).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=196620;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MW2;  
 RA MEDLINE=22040717; PubMed=12044378;  
 RA Baba T., Takeuchi F., Kuroda M., Aoki K.-I., Oguuchi A.,  
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,  
 RA Yamamoto K., Hiramatsu K.;  
 RT "Genome and virulence determinants of high virulence community-  
 RT acquired MRSA.";  
 RL Lancet 359:1819-1827 (2002).  
 DR EMBL; AP004823; BAB94318.1; -;  
 DR GO; GO:0030435; P:sporulation; IEA.  
 DR InterPro; IPR007170; SpovG.  
 DR Pfam; PF04026; SpovG; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 100 AA; 11278 MW; 876C2BC87CF7F4C CRC64;

## Query Match

100.0%; Score 26; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEVP 5  
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DB 84 DEVP 88

Search completed: December 8, 2004, 08:55:47  
 Job time : 65 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 08:48:48 ; Search time 37 Seconds

(without alignments)  
8.962 Million cell updates/sec

Title: SEQ1  
Perfect score: 26  
Sequence: 1 devp 5

Scoring table: BLOSUM62

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	26	100.0	5	4	US-09-728-653-8
3	26	100.0	6	4	US-10-015-328-5
4	26	100.0	6	4	US-10-015-328-7
5	26	100.0	6	4	US-10-015-328-11
6	26	100.0	6	4	US-09-728-653-5
7	26	100.0	6	4	US-09-728-653-7
8	26	100.0	6	4	US-09-728-653-11
9	26	100.0	125	2	US-08-862-480B-1
10	26	100.0	135	4	US-09-270-767-39928
11	26	100.0	135	4	US-09-270-767-39928
12	26	100.0	135	4	US-09-270-767-39928
13	26	100.0	135	4	US-09-270-767-39928
14	26	100.0	151	3	US-08-916-043-5
15	26	100.0	151	3	US-09-428-929-5
16	26	100.0	151	6	5212286-2
17	26	100.0	155	4	US-09-270-767-43954
18	26	100.0	181	4	US-09-270-767-60700
19	26	100.0	207	4	US-09-489-039A-11981
20	26	100.0	249	4	US-09-538-092-586
21	26	100.0	267	4	US-09-248-796A-14641
22	26	100.0	293	4	US-09-668-262A-12
23	26	100.0	351	4	US-09-248-796A-17247
24	26	100.0	379	4	US-09-538-092-2
25	26	100.0	416	4	US-09-270-767-45205
26	26	100.0	445	4	US-09-489-039A-9765
27	26	100.0	455	5	US-08-272-255-14

28	26	100.0	538	4	US-09-248-796A-20842	Sequence 20842, A
29	26	100.0	715	4	US-09-489-039A-12511	Sequence 12511, A
30	26	100.0	998	4	US-08-252-991A-24402	Sequence 24402, A
31	26	100.0	1171	4	US-09-489-039A-10298	Sequence 10298, A
32	26	100.0	1189	4	US-09-489-039A-13776	Sequence 13776, A
33	26	96.2	6	4	US-09-368-670C-11	Sequence 11, Appl
34	25	96.2	18	2	US-08-532-269B-9	Sequence 9, Appl
35	25	96.2	18	3	US-08-294-923-9	Sequence 21591, A
36	25	96.2	65	4	US-08-248-796A-21591	Sequence 3334, Ap
37	25	96.2	110	3	US-09-134-001C-3334	Sequence 51, Appl
38	25	96.2	121	2	US-08-576-626A-51	Sequence 16, Appl
39	25	96.2	149	4	US-09-735-846-4	Sequence 19755, A
40	25	96.2	150	4	US-09-735-846-6	Sequence 12, Appl
41	25	96.2	186	4	US-09-248-796A-19755	Sequence 98, Appl
42	25	96.2	194	4	US-09-735-846-6	
43	25	96.2	226	4	US-09-555-510B-12	
44	25	96.2	226	4	US-10-231-013-12	
45	25	96.2	264	4	US-09-602-787A-98	

## ALIGNMENTS

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RESULT 1
US-10-015-328-8
; Sequence 8, Application US/10015328
; Patent No. 6727366
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
; TITLE OF INVENTION: Protease Inhibitors
; FILE REFERENCE: PH-7203
; CURRENT APPLICATION NUMBER: US/10/015,328
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,168
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
; FEATURE:
; OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
; NAME/KEY: MOD RES
; LOCATION: (2)..(2)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-10-015-328-8

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5
DB 1 DEVP 5

RESULT 2
US-09-728-653-8
; Sequence 8, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
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APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease
FILE REFERENCE: PH-718
CURRENT APPLICATION NUMBER: US/09/728,653
CURRENT FILING DATE: 2000-12-01
PRIORITY FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
FEATURE:
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
NAME/KEY: MOD_RES
LOCATION: (2)..(2)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
US-09-728-653-8
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Query Match      100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DEVVP 5
Db      1 DEVVP 5
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## RESULT 3

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US-10-015-328-5
Sequence 5, Application US/10015328
Patent No. 6727366
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIORITY FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: Boro-allylglycine
US-10-015-328-5
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Query Match      100.0%; Score 26; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DEVVP 5
Db      1 DEVVP 5
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## RESULT 4

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US-10-015-328-7
Sequence 7, Application US/10015328
Patent No. 6727366
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIORITY FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-10-015-328-7
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Query Match      100.0%; Score 26; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DEVVP 5
Db      1 DEVVP 5
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## RESULT 5

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US-10-015-328-11
Sequence 11, Application US/10015328
Patent No. 6727366
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Han, Amy Qi
APPLICANT: Glunz, Peter W.
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus
FILE REFERENCE: PH-7203
CURRENT APPLICATION NUMBER: US/10/015,328
CURRENT FILING DATE: 2001-12-12
PRIORITY FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
FEATURE:
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl
NAME/KEY: MOD_RES
LOCATION: (2)..(2)
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
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; OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-10-015-328-11
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Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 6
US-09-728-653-5
; Sequence 5, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 6
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US-09-728-653-5

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 7
US-09-728-653-7
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; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
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US-09-728-653-7

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 8
US-09-728-653-11
; Sequence 11, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
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; OTHER INFORMATION: Delta-Carboxy Ester: t-Buyl
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; LOCATION: (2)..(2)
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Buyl
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-09-728-653-11

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 9
US-08-862-480B-1
; Sequence 1, Application US/08862480B
; Patent No. 5965533
; GENERAL INFORMATION:
; APPLICANT: Chen, Chi J.; Shockley, Ty R., and
; APPLICANT: Johnston, Miles G.
; TITLE OF INVENTION: Atrial Natriuretic Peptide
; TITLE OF INVENTION: Peritoneal Dialysis Solutions
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Thomas Borecki
; STREET: 1620 N. Waukegan Road
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; LOCATION: (6)..(6)
; OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-09-728-653-7
Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 8
US-09-728-653-11
; Sequence 11, Application US/09728653
; Patent No. 6774212
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Han, Amy Qi
; APPLICANT: Glunz, Peter W.
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease
; FILE REFERENCE: PH-7118
; CURRENT APPLICATION NUMBER: US/09/728,653
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,998
; PRIOR FILING DATE: 1999-12-03
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; NAME/KEY: MOD RES
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; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl
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; LOCATION: (2)..(2)
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; OTHER INFORMATION: Boro-allylglycine pinanediol ester
US-09-728-653-11

Query Match
Best Local Similarity 100.0%; Score 26; DB 4; Length 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5
Db 1 DEVP 5

RESULT 9
US-08-862-480B-1
; Sequence 1, Application US/08862480B
; Patent No. 5965533
; GENERAL INFORMATION:
; APPLICANT: Chen, Chi J.; Shockley, Ty R., and
; APPLICANT: Johnston, Miles G.
; TITLE OF INVENTION: Atrial Natriuretic Peptide
; TITLE OF INVENTION: Peritoneal Dialysis Solutions
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Thomas Borecki
; STREET: 1620 N. Waukegan Road
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CITY: McGaw Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60085  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,480B  
FILING DATE: 23-MAY-1997  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acid residues  
TYPE: amino acid  
STRANDEDNESS: No. 596553 Relevant  
TOPOLOGY: No. 596553 Relevant  
MOLECULE TYPE: peptide  
US-08-862-480B-1

Query Match 100.0%; Score 26; DB 2; Length 125;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
DB 30 DEVP 34

RESULT 10  
US-09-270-767-39928  
Sequence 39928, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 39928  
LENGTH: 135  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-39928

Query Match 100.0%; Score 26; DB 4; Length 135;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
DB 112 DEVP 116

RESULT 11  
US-09-270-767-55145  
Sequence 55145, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 55145  
LENGTH: 135  
TYPE: PRT

ORGANISM: Drosophila melanogaster  
US-09-270-767-55145

Query Match 100.0%; Score 26; DB 4; Length 135;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
DB 112 DEVP 116

RESULT 12  
5212286-4  
Patent No. 5212286  
APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR  
PEPTIDE COMPOUNDS  
NUMBER OF SEQUENCES: 68  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/870,795  
FILING DATE: 05-JUN-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 766,030  
FILING DATE: 08-MAY-1985  
APPLICATION NUMBER: 602,117  
FILING DATE: 09-APR-1984  
APPLICATION NUMBER: 616,488  
FILING DATE: 01-JUN-1984  
SEQ ID NO: 4  
LENGTH: 136  
5212286-4

Query Match 100.0%; Score 26; DB 6; Length 136;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
DB 40 DEVP 44

RESULT 13  
US-08-916-043-5  
Sequence 5, Application US/08916043  
Patent No. 6013630  
GENERAL INFORMATION:  
APPLICANT: Shimkets, Richard A.  
TITLE OF INVENTION: ATRIAL NATRIURETIC FACTOR MUTANTS  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/916,043  
FILING DATE: 21-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7934-048  
TELEPHONE: 212-790-9090  
TELEPHONE: 212-869-8864  
TELEPHONE: 212-869-8864



TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-916-043-5

Query Match 100.0%; Score 26; DB 3; Length 151;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5  
Db 55 DEVP 59

RESULT 14  
US-09-428-929-5  
Sequence 5, Application US/09428929  
Patent No. 6514939  
GENERAL INFORMATION:  
APPLICANT: Shinkens, Richard A.  
TITLE OF INVENTION: ATRIAL NATRIURETIC FACTOR MUTANTS  
TITLE OF INVENTION: AND ISCHEMIC STROKE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/428,929  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/916,043  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7934-048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-428-929-5

Query Match 100.0%; Score 26; DB 4; Length 151;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5  
Db 55 DEVP 59

RESULT 15

5212286-2  
Patent No. 5212286  
APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR  
PEPTIDE COMPOUNDS  
NUMBER OF SEQUENCES: 68  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/870,795  
FILING DATE: 05-JUN-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 766,030  
FILING DATE: 08-MAY-1985  
APPLICATION NUMBER: 602,117  
FILING DATE: 09-APR-1984  
APPLICATION NUMBER: 616,488  
FILING DATE: 01-JUN-1984  
SEQ ID NO: 2:  
LENGTH: 151  
5212286-2

Query Match 100.0%; Score 26; DB 6; Length 151;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5  
Db 55 DEVP 59

Search completed: December 8, 2004, 08:57:13  
Job time : 38 secs

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OM protein - protein search, using SW model

Run on: December 8, 2004, 08:52:01 ; Search time 143 Seconds

(without alignments)  
12.489 Million cell updates/sec

Title: SEQ1

Perfect score: 26

Sequence: 1 decomp 5

Scoring table:

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Searched:

1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	26	100.0	5	14	US-10-015-328-8
3	26	100.0	6	9	US-09-728-653-5
4	26	100.0	6	9	US-09-728-653-7
5	26	100.0	6	9	US-09-728-653-11
6	26	100.0	6	14	US-10-010-184A-5
7	26	100.0	6	14	US-10-015-328-5
8	26	100.0	6	14	US-10-015-328-7
9	26	100.0	6	14	US-10-015-328-11
10	26	100.0	9	14	US-10-133-133A-10
11	26	100.0	9	14	US-10-133-133A-20
12	26	100.0	67	17	US-10-425-115-234557
13	26	100.0	71	15	US-10-424-599-285243

14	26	100.0	78	9	US-09-795-501-10	Sequence 10, Appl
15	26	100.0	81	16	US-10-437-963-135073	Sequence 135073,
16	26	100.0	91	16	US-10-437-963-193303	Sequence 193303,
17	26	100.0	96	16	US-10-437-963-173337	Sequence 173337,
18	26	100.0	109	17	US-10-425-115-204973	Sequence 204973,
19	26	100.0	120	13	US-10-036-444-4	Sequence 4, Appl
20	26	100.0	120	16	US-10-767-701-41220	Sequence 41220, A
21	26	100.0	121	16	US-10-767-701-40460	Sequence 40460, A
22	26	100.0	123	15	US-10-425-115-229771	Sequence 229771,
23	26	100.0	124	15	US-10-424-599-272233	Sequence 272233,
24	26	100.0	125	15	US-10-392-837A-3	Sequence 3, Appl
25	26	100.0	126	14	US-10-419-059-3	Sequence 3, Appl
26	26	100.0	126	16	US-10-645-874-3	Sequence 3, Appl
27	26	100.0	129	15	US-10-424-599-158168	Sequence 158168,
28	26	100.0	130	15	US-10-392-837A-4	Sequence 4, Appl
29	26	100.0	130	15	US-10-392-837A-5	Sequence 5, Appl
30	26	100.0	130	15	US-10-392-837A-6	Sequence 6, Appl
31	26	100.0	135	15	US-10-333-481-17	Sequence 17, Appl
32	26	100.0	145	16	US-10-767-701-52098	Sequence 52098, A
33	26	100.0	151	14	US-10-419-059-4	Sequence 4, Appl
34	26	100.0	151	16	US-10-645-874-4	Sequence 4, Appl
35	26	100.0	153	14	US-10-201-288-17	Sequence 17, Appl
36	26	100.0	161	16	US-10-696-259-10	Sequence 10, Appl
37	26	100.0	162	15	US-10-425-114-37635	Sequence 37635, A
38	26	100.0	163	17	US-10-425-115-317745	Sequence 317745,
39	26	100.0	167	17	US-10-425-115-344226	Sequence 344226,
40	26	100.0	170	16	US-10-437-963-173977	Sequence 173977,
41	26	100.0	171	15	US-10-425-114-48819	Sequence 48819, A
42	26	100.0	175	16	US-10-696-259-8	Sequence 8, Appl
43	26	100.0	177	16	US-10-696-259-5	Sequence 5, Appl
44	26	100.0	185	16	US-10-696-259-7	Sequence 7, Appl
45	26	100.0	190	13	US-10-036-444-2	Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-09-728-653-8  
Sequence 8, Application US/09728653  
Publication No. US20020123468A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
TITLE OF INVENTION: Alpha-Ketamide Inhibitors of Hepatitis C Virus NS3 Protease  
FILE REFERENCE: PR-7118  
CURRENT APPLICATION NUMBER: US/09/728,653  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 60/168,998  
PRIOR FILING DATE: 1999-12-03  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MOD\_RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl  
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (2)..(2)  
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl  
US-09-728-653-8  
Query Match 100.0%; Score 26; DB 9; Length 5;  
Best local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
11111  
Db 1 DEVP 5

RESULT 2  
US-10-015-328-8

; Sequence 8, Application US/10015328  
; Publication No. US20030100768A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; APPLICANT: Han, Amy Qi  
; APPLICANT: Glunz, Peter W.  
; TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Virus  
; FILE REFERENCE: PH-7203  
; CURRENT APPLICATION NUMBER: US/10/015,328  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,168  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl  
; FEATURE:  
; OTHER INFORMATION: Delta-Carboxy Ester: t-Buyl  
; NAME/KEY: MOD RES  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: Gamma-Carboxy Ester: t-Buyl  
US-10-015-328-8

Query Match 100.0%; Score 26; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
11111  
Db 1 DEVP 5

RESULT 3

US-09-728-653-5  
; Sequence 5, Application US/09728653  
; Publication No. US20020123468A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; APPLICANT: Han, Amy Qi  
; APPLICANT: Glunz, Peter W.  
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease  
; FILE REFERENCE: PH-7118  
; CURRENT APPLICATION NUMBER: US/09/728,653  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/168,998  
; PRIOR FILING DATE: 1999-12-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
; NAME/KEY: MISC\_FEATURE

; LOCATION: (6)..(6)  
; OTHER INFORMATION: Boro-allylglycine  
US-09-728-653-5

Query Match 100.0%; Score 26; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
11111  
Db 1 DEVP 5

RESULT 4

US-09-728-653-7  
; Sequence 7, Application US/09728653  
; Publication No. US20020123468A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; APPLICANT: Han, Amy Qi  
; APPLICANT: Glunz, Peter W.  
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease  
; FILE REFERENCE: PH-7118  
; CURRENT APPLICATION NUMBER: US/09/728,653  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/168,998  
; PRIOR FILING DATE: 1999-12-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: Boro-allylglycine pinanediol ester  
US-09-728-653-7

Query Match 100.0%; Score 26; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
11111  
Db 1 DEVP 5

RESULT 5

US-09-728-653-11  
; Sequence 11, Application US/09728653  
; Publication No. US20020123468A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; APPLICANT: Han, Amy Qi  
; APPLICANT: Glunz, Peter W.  
; TITLE OF INVENTION: Alpha-Ketoamide Inhibitors of Hepatitis C Virus NS3 Protease  
; FILE REFERENCE: PH-7118  
; CURRENT APPLICATION NUMBER: US/09/728,653  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/168,998  
; PRIOR FILING DATE: 1999-12-03  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
; NAME/KEY: MISC\_FEATURE

NAME/KEY: MOD RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl  
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (2)..(2)  
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (6)..(6)  
OTHER INFORMATION: Boro-allylglycine pinanediol ester  
US-09-728-653-11

Query Match 100.0%; Score 26; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
Db 1 DEVVP 5

RESULT 6  
US-10-010-184A-5  
Sequence 5, Application US/10010184A  
Publication No. US20030008828A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Pharma Company  
APPLICANT: Priestly, et al.  
TITLE OF INVENTION: No. US20030008828A1 Lactam Inhibitors of Hepatitis C Virus NS3  
FILE REFERENCE: PH-7087-A  
CURRENT APPLICATION NUMBER: US/10/010,184A  
CURRENT FILING DATE: 2002-05-17  
PRIOR APPLICATION NUMBER: US 09/626,286  
PRIOR FILING DATE: 2000-07-25  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 43A pept  
OTHER INFORMATION: ide synthesizer using readily available materials well known to c  
OTHER INFORMATION: rdinarily skilled artisans  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (6)..(6)  
OTHER INFORMATION: 2-amino-4-penten-boronic acid  
US-10-010-184A-5

Query Match 100.0%; Score 26; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
Db 1 DEVVP 5

RESULT 7  
US-10-015-328-5  
Sequence 5, Application US/10015328  
Publication No. US20030100768A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Vir  
FILE REFERENCE: PH-7203  
CURRENT APPLICATION NUMBER: US/10/015,328

CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 60/255,168  
PRIOR FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MISC FEATURE  
LOCATION: (6)..(6)  
OTHER INFORMATION: Boro-allylglycine  
US-10-015-328-5

Query Match 100.0%; Score 26; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
Db 1 DEVVP 5

RESULT 8  
US-10-015-328-7  
Sequence 7, Application US/10015328  
Publication No. US20030100768A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Vir  
FILE REFERENCE: PH-7203  
CURRENT APPLICATION NUMBER: US/10/015,328  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 60/255,168  
PRIOR FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
NAME/KEY: MISC FEATURE  
LOCATION: (6)..(6)  
OTHER INFORMATION: Boro-allylglycine pinanediol ester  
US-10-015-328-7

Query Match 100.0%; Score 26; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
Db 1 DEVVP 5

RESULT 9  
US-10-015-328-11  
Sequence 11, Application US/10015328  
Publication No. US20030100768A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
APPLICANT: Han, Amy Qi  
APPLICANT: Glunz, Peter W.  
TITLE OF INVENTION: Imidazolidinones and Their Related Derivatives as Hepatitis C Vir

TITLE OF INVENTION: Protease Inhibitors  
FILE REFERENCE: PH-7203  
CURRENT APPLICATION NUMBER: US/10/015,328  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 60/255,168  
PRIOR FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized by standard organic chemistry laboratory methods.  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (1)-(1)  
OTHER INFORMATION: N-terminal Protecting Group: t-Butoxycarbonyl  
OTHER INFORMATION: Delta-Carboxy Ester: t-Butyl  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (2)-(2)  
OTHER INFORMATION: Gamma-Carboxy Ester: t-Butyl  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (6)-(6)  
OTHER INFORMATION: Boro-allylglycine pinanediol ester  
US-10-015-328-11

Query Match 100.0%; Score 26; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
Db 1 DEVVP 5

RESULT 10  
US-10-133-133A-10  
Sequence 10, Application US/10133133A  
Publication No. US20030114385A1  
GENERAL INFORMATION:  
APPLICANT: CATHERS, Brian  
APPLICANT: NEUTERBOON, Saskia  
APPLICANT: SHEPARD, Michael  
TITLE OF INVENTION: VIRAL ENZYME ACTIVATED PROTOXOPHORES  
TITLE OF INVENTION: AND USE OF SAME TO TREAT VIRAL INFECTIONS  
FILE REFERENCE: NB 2021.00  
CURRENT APPLICATION NUMBER: US/10/133,133A  
CURRENT FILING DATE: 2002-04-26  
PRIOR APPLICATION NUMBER: 60/286,983  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide sequence attached to prodrug compound  
OTHER INFORMATION: activated by hepatitis C virus NS3 protease  
FEATURE:  
NAME/KEY: ACETYLTATION  
LOCATION: (1)...(10)  
US-10-133-133A-10

Query Match 100.0%; Score 26; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5

Db 1 DEVVP 5  
RESULT 11  
US-10-133-133A-20  
Sequence 20, Application US/10133133A  
Publication No. US20030114385A1  
GENERAL INFORMATION:  
APPLICANT: CATHERS, Brian  
APPLICANT: NEUTERBOON, Saskia  
APPLICANT: SHEPARD, Michael  
TITLE OF INVENTION: VIRAL ENZYME ACTIVATED PROTOXOPHORES  
TITLE OF INVENTION: AND USE OF SAME TO TREAT VIRAL INFECTIONS  
FILE REFERENCE: NB 2021.00  
CURRENT APPLICATION NUMBER: US/10/133,133A  
CURRENT FILING DATE: 2002-04-26  
PRIOR APPLICATION NUMBER: 60/286,983  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide sequence attached to prodrug compound  
OTHER INFORMATION: activated by hepatitis C virus NS3 protease  
FEATURE:  
NAME/KEY: ACETYLTATION  
LOCATION: (1)...(10)  
US-10-133-133A-20

Query Match 100.0%; Score 26; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
Db 1 DEVVP 5

RESULT 12  
US-10-425-115-234557  
Sequence 234557, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 234557  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(67)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_145501C.1.pcp  
US-10-425-115-234557

Query Match 100.0%; Score 26; DB 17; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5

Db 33 DEVP 37

## RESULT 13

US-10-424-599-285243  
 ; Sequence 285243, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 285243  
 ; LENGTH: 71  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_99603C.1.pep  
 US-10-424-599-285243

Query Match 100.0%; Score 26; DB 15; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5

Db 60 DEVP 64

## RESULT 14

US-09-795-501-10  
 ; Sequence 10, Application US/09795501  
 ; Patent No. US20020042098A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: Meyers, Rachel  
 ; TITLE OF INVENTION: 32253 TRANSFERASE FAMILY MEMBERS AND  
 ; FILE REFERENCE: 38155-20004.00  
 ; CURRENT APPLICATION NUMBER: US/09/795,501  
 ; CURRENT FILING DATE: 2001-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/185,755  
 ; PRIOR FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 78  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Consensus amino acid sequence  
 US-09-795-501-10

Query Match 100.0%; Score 26; DB 9; Length 78;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5

Db 4 DEVP 8

## RESULT 15

US-10-437-963-135073  
 ; Sequence 135073, Application US/10437963  
 ; Publication No. US20040123343A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 135073  
 ; LENGTH: 81  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_36784C.1.pep  
 US-10-437-963-135073

Query Match 100.0%; Score 26; DB 16; Length 81;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5

Db 43 DEVP 47

Search completed: December 8, 2004, 08:59:42  
 Job time: 143 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 8, 2004, 08:34:26 ; Search time 38 Seconds

(without alignments)  
12.660 Million cell updates/sec

Title: SEQ1  
Perfect score: 26  
Sequence: 1 decomp 5

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 79;.\*  
2: PIR1;.\*  
3: PIR2;.\*  
4: PIR3;.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	42	2	G69113
2	26	100.0	74	2	T19911
3	26	100.0	102	2	T07890
4	26	100.0	108	2	C89816
5	26	100.0	129	2	F87109
6	26	100.0	150	2	AC3294
7	26	100.0	151	1	AMHU
8	26	100.0	152	2	AC3598
9	26	100.0	162	2	T29728
10	26	100.0	170	2	AD0114
11	26	100.0	176	2	E95274
12	26	100.0	208	2	G87475
13	26	100.0	214	2	AB2195
14	26	100.0	225	2	SS7810
15	26	100.0	249	2	SS5904
16	26	100.0	287	2	T32029
17	26	100.0	289	2	S38770
18	26	100.0	289	2	S17161
19	26	100.0	301	2	C64448
20	26	100.0	327	2	T42999
21	26	100.0	340	2	T47371
22	26	100.0	344	2	AG2882
23	26	100.0	346	2	F97658
24	26	100.0	361	2	AP3560
25	26	100.0	365	2	T37720
26	26	100.0	366	2	A11327
27	26	100.0	366	2	AC1699
28	26	100.0	377	2	T46149
29	26	100.0	393	2	S72804

30	26	100.0	393	2	S23409	FUN20 protein - ye
31	26	100.0	395	2	S75952	hypothetical prote
32	26	100.0	399	2	G75332	acetyl-CoA acetyl
33	26	100.0	411	2	S26195	probable carboxyl-
34	26	100.0	418	2	T39230	hypothetical prote
35	26	100.0	419	2	AG0046	probable membrane
36	26	100.0	424	1	XNBYP	choline-phosphate
37	26	100.0	432	2	T30597	enoyl-CoA hydratase
38	26	100.0	433	2	T48118	hypothetical prote
39	26	100.0	436	2	T00756	hypothetical prote
40	26	100.0	449	2	D69476	TBP-interacting pr
41	26	100.0	450	2	E98303	hypothetical 49.3K
42	26	100.0	450	2	AB2979	ultraviolet-sensitive
43	26	100.0	455	2	S05573	deoxyribodipyrimid
44	26	100.0	460	2	T47108	serine-tRNA ligase
45	26	100.0	467	2	E69601	ATP-dependent Clp

#### ALIGNMENTS

##### RESULT 1

G69113  
hypothetical protein MTH1845 - Methanobacterium thermoautotrophicum (strain Delta H)  
C/Species: Methanobacterium thermoautotrophicum  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: G69113  
R/Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
A/Reference number: A69000; M01D:98037514; PMID:9371463  
A/Accession: G69113  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-42 <MTH>  
A/Cross-references: UNIPROT:Q27873; GB:AB000937; GB:AE000666; MID:G2622974; PIDN:AB86311  
A/Experimental source: strain Delta H  
C/Genetics:  
A/Genes: MTH1845

Query Match 100.0%; Score 26; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 13;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5

DB 35 DEVVP 39

##### RESULT 2

T19911  
hypothetical protein C43F9.7 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T19911

R/Morimore, B.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z19195

A/Accession: T19911

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-74 <MTH>

A/Cross-references: UNIPROT:Q9XUG8; EMBL:Z82262; PIDN:CAB05150.1; GSPDB:GN00022; CESP:C4

A/Experimental source: clone C43F9

C/Genetics:  
A/Genes: CESP:C43F9.7  
A/Map position: 4  
A/Introns: 23/1; 47/2

Query Match 100.0%; Score 26; DB 2; Length 74;  
Best Local Similarity 100.0%; Pred. No. 25;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVP 5  
 |||||  
 Db 30 DEVP 34

## RESULT 3

T07890  
 protein kinase (BC 2.7.1.-) 5 - tomato (fragment)  
 C/Species: Lycopersicon esculentum (tomato)  
 C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 16-Aug-2004  
 C/Accession: T07890  
 R/Zhang, S.; Diener, T.O.  
 Submitted to the EMBL Data Library, February 1997  
 A/Description: Isolation and characterization of seven serine/threonine protein kinase-c  
 A/Reference number: Z16191  
 A/Accession: T07890  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-102 <ZHA>  
 A/Cross-references: UNIPROT:Q49991; EMBL:U89682; NID:g2735253; PIDN:AAB93863.1; PID:g273  
 A/Experimental source: cultivar Rutgers; seedling  
 C/Genetics:  
 A/Gene: PK5  
 C/Superfamily: protein kinase homology  
 C/Keywords: phosphotransferase

Query Match 100.0%; Score 26; DB 2; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 |||||  
 Db 27 DEVP 31

## RESULT 4

C89816  
 hypothetical protein spovg [imported] - Staphylococcus aureus (strain N315)  
 C/Species: Staphylococcus aureus  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C/Accession: C89816  
 R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
 ma, A.; Mizutani-Ut, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratazu, K.  
 Lancet 357, 1225-1240, 2001  
 A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
 A/Reference number: A89758; MUID:21311952; PMID:11418146  
 A/Accession: C89816  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-108 <KUR>  
 A/Cross-references: UNIPROT:Q99WA5; GB:BA000018; PID:g13700388; PIDN:BA841686.1; GSPDB:G  
 A/Experimental source: strain N315  
 C/Genetics:  
 A/Gene: spovg  
 C/Superfamily: stage V sporulation protein spovg

Query Match 100.0%; Score 26; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 |||||  
 Db 92 DEVP 96

## RESULT 5

F87109  
 hypothetical protein [imported] - Mycobacterium leprae  
 C/Species: Mycobacterium leprae  
 C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

C/Accession: F87109  
 R/Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor  
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holtroyd,  
 eam, M.A.; Rutherford, K.M  
 Nature 409, 1007-1011, 2001  
 A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq  
 A/Title: Massive gene decay in the leprosy bacillus.  
 A/Reference number: A86909; MUID:21128732; PMID:11234002  
 A/Accession: F87109  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-129 <STO>  
 A/Cross-references: UNIPROT:Q9CBT7; GB:AL450380; NID:g13093395; PIDN:CA030555.1; GSPDB:G  
 C/Genetics:  
 A/Gene: ML1604

Query Match 100.0%; Score 26; DB 2; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 |||||  
 Db 22 DEVP 26

## RESULT 6

AC3294  
 biopolymer transport exbd protein [imported] - Brucella melitensis (strain 16M)  
 C/Species: Brucella melitensis  
 C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C/Accession: AC3294  
 R/Divechko, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I  
 Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Levesc  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis;  
 A/Reference number: AD3252; PMID:11756688  
 A/Accession: AC3294  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-150 <KUR>  
 A/Cross-references: UNIPROT:O8YIV3; GB:AE008917; PIDN:AAL51518.1; PID:g17982233; GSPDB:G  
 A/Experimental source: strain 16M  
 C/Genetics:  
 A/Gene: BMEI0337  
 A/Map position: 1  
 C/Superfamily: tolR protein

Query Match 100.0%; Score 26; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 |||||  
 Db 94 DEVP 98

## RESULT 7

AMH1  
 natriuretic peptide A precursor [validated] - human  
 N/Alternate names: ANP; atrial natriuretic factor; atrial natriuretic protein; prepronat  
 N/Contains: atrial alpha natriuretic peptide (ANP); cardiodilatin (atrial gamma natriuret  
 C/Species: Homo sapiens (man)  
 C/Date: 15-Nov-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
 C/Accession: A22693; B22693; A01424; B29370; A22733; I58054; S14097; I39458; I39459; I39  
 R/Nemer, M.; Chamberland, M.; Sirois, D.; Argentin, S.; Drouin, J.; Dixon, R.A.F.; Zivin  
 Nature 312, 654-656, 1984  
 A/Title: Gene structure of human cardiac hormone precursor, pronatriodilatin.  
 A/Reference number: A22693; MUID:85061626; PMID:6095118  
 A/Accession: A22693  
 A/Molecule type: DNA  
 A/Residues: 1-151 <NEM>  
 A/Cross-references: UNIPROT:P01160; GB:X01470; NID:g28687; PIDN:CAA25699.1; PID:g825625  
 A/Accession: B22693

A:Molecule type: DNA  
 A:Residues: 1-151, 'RR' <NE2>  
 A>Note: allelic variant with UGA termination codon replaced by CGA arginine codon  
 R:Okawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.; Nakazato, H.; Kangawa, K.; Fujita, 309, 724-726, 1984  
 A>Title: Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic factor  
 A:Reference number: A01424; MUID:84129199; PMID:6030342  
 A:Accession: A01424  
 A:Molecule type: mRNA  
 A:Residues: 1-151 <OK>  
 A:Cross-references: GB:K02043; NID:g178629; PIDN:AA59379.1; PID:g178630  
 R:Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, J.G.  
 Science 226, 1206-1209, 1984  
 A>Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.  
 A:Reference number: A29370; MUID:85065766; PMID:6542248  
 A:Accession: B29370  
 A:Molecule type: DNA  
 A:Residues: 1-64, 'D', '66-151' <SE1>  
 A:Cross-references: GB:K02043  
 R:Kangawa, K.; Matsuo, H.  
 Biochem. Biophys. Res. Commun. 118, 131-139, 1984  
 A>Title: Purification and complete amino acid sequence of alpha-human atrial natriuretic factor  
 A:Reference number: A32733; MUID:84128019; PMID:6230082  
 A:Accession: A32733  
 A:Molecule type: protein  
 A:Residues: 124-151 <KAN>  
 R:Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S.  
 Nature 310, 699-701, 1984  
 A>Title: mRNA sequence for human cardiolipin-atrial natriuretic factor precursor and  
 A:Reference number: 158054; MUID:84295577; PMID:6547996  
 A:Accession: 158054  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-151 <RES>  
 A:Cross-references: GB:M30262; NID:g180181; PIDN:AAA35669.1; PID:g180182  
 R:Vansteede, Y.; Michel, A.; Deschodt-Lanckman, M.  
 Eur. J. Biochem. 196, 281-286, 1991  
 A>Title: Hydrolysis of intact and Cys-Phe-cleaved human atrial natriuretic peptide in vitro  
 A:Reference number: S14097; MUID:91176996; PMID:1826098  
 A:Accession: S14097  
 A:Molecule type: protein  
 A:Residues: 124-151 <VAN>  
 A>Note: natural and synthetic peptide subjected to kallikrein proteolysis  
 R:Zivin, R.A.; Conda, J.H.; Dixon, R.A.; Seidman, M.G.; Chretien, M.; Nemer, M.; Chamber  
 Proc. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984  
 A>Title: Molecular cloning and characterization of DNA sequences encoding rat and human  
 A:Reference number: I39458; MUID:85038509; PMID:6238331  
 A:Accession: I39458  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 119-151, 'RR' <RE2>  
 A:Cross-references: GB:K02044; NID:g178631; PIDN:AAA51730.1; PID:g178632  
 R:Maki, M.; Parmentier, M.; Inagami, T.  
 Biochem. Biophys. Res. Commun. 125, 797-802, 1984  
 A>Title: Cloning of genomic DNA for human atrial natriuretic factor.  
 A:Reference number: I39459; MUID:850696983; PMID:6097248  
 A:Accession: I39459  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-75 <RE3>  
 A:Cross-references: GB:K02399; NID:g178633; PIDN:AAA5528.1; PID:g178634  
 R:Seidman, C.E.; Bloch, K.D.; Zisfein, J.; Smit, J.; Haber, E.; Homcy, C.J.; Duby, A.D.;  
 Hypertension 7, 31-34, 1985  
 A>Title: Molecular studies of the atrial natriuretic factor gene.  
 A:Reference number: I39460  
 A:Accession: I39460  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-64, 'D', '66-151' <RE4>  
 A:Cross-references: GB:M54951; NID:g178636; PIDN:AAA35529.1; PID:g178638  
 R:Greenberg, B.D.; Bencen, G.H.; Sellhammer, J.J.; Lewicki, J.A.; Fiddes, J.C.  
 Nature 312, 656-658, 1984  
 A>Title: Nucleotide sequence of the gene encoding human atrial natriuretic factor precu

A:Reference number: I37167; MUID:85061627; PMID:6095119  
 A:Accession: I37167  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 26-151 <RE5>  
 A:Cross-references: EMBL:X01471; NID:g28690; PIDN:CAA25700.1; PID:g1340150  
 C:Comment: Cardiolipin is a vasoconstrictor but not a diuretic or natriuretic.  
 C:Genetics:  
 A:Gene: GDB:NPPA; ANP; PND  
 A:Cross-references: GDB:I18727; OMIM:108780  
 A:Map position: Ip36-Ip36  
 A:Introns: 41/3; 150/3  
 C:Superfamily: natriuretic peptide A precursor  
 C:Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation  
 F:126-151/Product: signal sequence #status predicted <SIG>  
 F:124-151/Product: cardiolipin #status predicted <SIG>  
 F:130-146/Disulfide bonds: #status experimental

Query Match 100.0%; Score 26; DB 1; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5  
 Db 55 DEVP 59

RESULT 8  
 AC3598  
 ebsc protein [imported] - Brucella melitensis (strain 16M)  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C:Accession: AC3598

R:Delvecchio, V.G.; Kaput, V.; Redkar, R.J.; Patra, G.; Mojter, C.; Los, T.; Ivanova,  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A:Reference number: AD3552; PMID:11756688  
 A:Accession: AC3598  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-152 <KIR>  
 A:Cross-references: UNIPROT:Q8YCS5; GB:AE008918; PIDN:AAL53950.1; PID:g17984896; GSPDB:C.C  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEI10708  
 A:Map position: II

Query Match 100.0%; Score 26; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVP 5  
 Db 119 DEVP 123

RESULT 9  
 T29728  
 hypothetical protein K0394.7 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 R:Du, Z.; Le, T.T.; Kemp, K.  
 submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of C. elegans cosmid K0394.  
 A:Reference number: Z20673  
 A:Accession: T29728

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-162 <DUT>  
 A:Cross-references: UNIPROT:Q21175; EMBL:U55370; PIDN:AAA97999.1; GSPDB:GN00023; CESP:KO:

A:Experimental source: strain Bristol N2; clone K03B4  
 C:Genetics:  
 A:Gene: CESP:K03B4.7  
 A:Map position: 5  
 A:Introns: 58/3; 105/3

Query Match 100.0%; Score 26; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 DB 22 DEVP 26

## RESULT 10

AD0114  
 conserved hypothetical protein YPO0932 [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*  
 C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: AD0114  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, Nature 413, 523-527, 2001  
 A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AD0114  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-170 <KUR>  
 A:Cross-references: UNIPROT:Q8ZH66; GB:AL590842; PIDN:CN09775.1; PID:q15979002; GSPDB:C  
 C:Genetics:  
 A:Gene: YPO0932  
 C:Superfamily: hypothetical protein H1173

Query Match 100.0%; Score 26; DB 2; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 DB 73 DEVP 77

## RESULT 11

E95274  
 hypothetical protein SMA0191 [imported] - *Sinorhizobium meliloti* (strain 1021) magaplast  
 C:Species: *Sinorhizobium meliloti*  
 C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
 C:Accession: E95274  
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
 A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*  
 A:Reference number: A95262; MUID:21396509; PMID:11481432  
 A:Accession: E95274  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-176 <KUR>  
 A:Cross-references: UNIPROT:Q9A0U3; GB:AE006469; PIDN:AAK64759.1; PID:g14523165; GSPDB:C  
 A:Experimental source: strain 1021, megaplastid pSymA  
 R:Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 P.; Chain, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A:Reference number: A96039; MUID:2136234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: SMA0191

A:Genome: plasmid

Query Match 100.0%; Score 26; DB 2; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 DB 62 DEVP 66

## RESULT 12

G87475  
 conserved hypothetical protein CCI828 [imported] - *Caulobacter crescentus*

C:Species: *Caulobacter crescentus*  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
 C:Accession: G87475  
 R:Neuman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.  
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolm  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A:Title: Complete Genome Sequence of *Caulobacter crescentus*.  
 A:Reference number: A87249; MUID:21173698; PMID:11259647  
 A:Accession: G87475  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-208 <STD>  
 A:Cross-references: UNIPROT:Q9A798; GB:AE005673; NID:g13423265; PIDN:AAK23803.1; GSPDB:G  
 C:Genetics:  
 A:Gene: CCI828

Query Match 100.0%; Score 26; DB 2; Length 208;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 DB 14 DEVP 18

## RESULT 13

AB2195  
 serine esterase [imported] - *Nostoc* sp. (strain PCC 7120)

C:Species: *Nostoc* sp. PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AB2195  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi  
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*  
 A:Reference number: AB1807; MUID:21595285; PMID:11758840  
 A:Accession: AB2195  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-214 <KUR>  
 A:Cross-references: UNIPROT:Q8YSH2; GB:BA000019; PIDN:BA074812.1; PID:g17132207; GSPDB:G  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: al13113

Query Match 100.0%; Score 26; DB 2; Length 214;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVP 5  
 DB 164 DEVP 168

## RESULT 14

hypothetical protein precursor (clone TPP11) - tomato

C/Species: Lycopersicon esculentum (tomato)  
 C/Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
 C/Accession: S57810  
 R/Milligan, S.B.; Gasser, C.S.  
 Plant Mol. Biol. 28, 691-711, 1995  
 A/Title: Nature and regulation of pIsf1-expressed genes in tomato.  
 A/Reference number: S57808; MUID:95375233; PMID:7647301  
 A/Accession: S57810  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-225 <MIL>  
 A/Cross-references: UNIPROT:Q04129; EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:99246  
 C/Superfamily: plant Kunitz-type proteinase inhibitor

Query Match 100.0%; Score 26; DB 2; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 87;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 |||||  
 Db 32 DEVVP 36

## RESULT 15

S59404  
 hypothetical protein YLR435w - yeast (Saccharomyces cerevisiae)  
 N/Alternate names: hypothetical protein L9753.3  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 30-Nov-1995 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
 C/Accession: S59404  
 R/Du, Z.  
 submitted to the EMBL Data Library, February 1995  
 A/Description: The sequence of S. cerevisiae cosmid 9753.  
 A/Reference number: S59401  
 A/Accession: S59404  
 A/Molecule type: DNA  
 A/Residues: 1-249 <DUZ>  
 A/Cross-references: UNIPROT:Q06672; EMBL:U21094; NID:9665967; PIDN:AAB67515.1; PID:96659  
 A/Experimental source: strain S288C (AB972)  
 C/Genetics:  
 A/Gene: MIPS:YLR435w  
 A/Cross-references: SGD:S0004427  
 A/Map position: 12R

Query Match 100.0%; Score 26; DB 2; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVVP 5  
 |||||  
 Db 218 DEVVP 222

Search completed: December 8, 2004, 08:56:31  
 Job time : 41 secs

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